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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Compugen Ltd.
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AF089868 Homo sapi
M29277 Human MC18
M2882 Human MC18
AB035506 Rattus no
AB035506 Rattus no
AB035509 Mus muscu
AB035509 Mus muscu
AB035509 Mus muscu
AB035509 Hisapiens M
X68267 H. sapiens M
AP00103 Homo sapi
Y08856 G.gallus mR
D38559 Chicken mRN
AP00103 Homo sapi
AP0011557 Homo sapi
AP001155 Homo sapi
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AP01156 Homo sapi
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Database

GenEmbl: *

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gb_ba2:*

gb_pl1:* gb_pl2:*

gb_ph: gb_ov: gb_om:*

gb_pr2:*

gb_prl:*

gb_sy:*

gb_ro:* gb_pr3:*

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Scoring table:

Title: Perfect score:

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MUC18 glycoprotein; cell adhesion molecule;
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Lehmann, J.M., Riethmuller, G. and Johnson, J.P. MC18, a marker of tumor progression in human me sequence similarity to the neural cell adhesion inmunoglobulin superfamily
Proc. Natl. Acad. Sci. U.S.A. 86 (24), 9891-9895
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Submitted (06-OCT-1989)
Immunology, University (
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IN GIYCOPTOTEIN MKNA, COMPLETE CO GI:529723 coprotein; cell adhesion molecule integral membrane glycoprotein. A to mRNA.	ACC VER KEYI SOU
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1861 atgggcetcctgcagggcagcagcggtgacaagagggctccggggagaccagg	Дy
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Throntogy, University of
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1 (bases 1 to 3306)

Lehmann, J.M., Riethmuller, G. and Johnson, J.P.

MUC18, a marker of tumor progression in human melanoma, shows sequence similarity to the neural cell adhesion molecules of the immunoglobulin superfamily

Proc. Natl. Acad. Sci. U.S.A. 86 (24), 9891-9895 (1989)
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Rattus norvegicus (strain:Sprague-Dawley) male
Rattus norvegicus
                                          AB035506 2106 bp
Rattus norvegicus mRNA
AB035506 1 GI:10566948
Eukaryota;
Metazoa;
Chordata;
                                                                 mRNA ROD for 1-gicerin/MUC18,
Craniata;
 Vertebrata;
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Taira,E., Okumura,S. and Miki,N.
Functional analysis of rat gicerin/MUC18
Published only in DataBase (2000) In pres
2 (bases 1 to 2106)
Taira,E., Okumura,S. and Miki,N.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-DEC-1999) to the DDBJ/EMBL/GenBank databases. Eiichi Taira, Osaka University Medical School, Department of Pharmacology 2-2 Yamada-oka, Suita, Osaka 565-0871, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (E-mail:etaira@pharmal.med.osaka-u.ac.jp,
Fax:+81-6-6879-3521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="1"gicerin/MUC18"
/product="1"gicerin/MUC18"
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/db_xref="GI 10566949"
/db_xref="GI 10566949"
/translation="MGLPRLVCAFLFAACCCCRSATGVPGEEKQPTPTPDPVEVEVGN
TALLKCGPAHPSGNFSQVEWFLIHKERQIPIFRVHQGKGOSEPGEYEHRLSLHGPGAT
LALSQVTPHDDRMFLCKSKQPRPODHYVOLQVYKAPEEPTIQANVLGIHVVIQELKEV
ATCVGRMGYPTPQVIHVYKNGRFED;QEENRHVH1QSSQTVESSGLYTKSVLSARVVKED
KDAQFYCEVSYRPPSGNRMKESKEVTVPVLYPAEKVWVEVEPVGLLKEGDHVKIRCLT
DGNPQPHFTINKKNPSTBEMEEESTDENGLLSLEPAQKHHSGVYQCQSLDLETTVMLS
SDPLELLVNYVSDVQVDPTAPEVQEGDSLTLTCKAESNQDLEFEWLRDKTGQLLGKGP
ILQLNNVKREAGGRYLCVASVPSVPGLNRTRRVSVGIFGSSWMAAKERKVWAQENAML
NLSCEASGHPQPTISWNINGSATEWNDPQTVSTLNLLVTPELLETGAECTASNSLG
SYTTVIILKLVTTTLTHDSSQTTGLSTPTVSPHSRANSTSTEKKLPQGESKGVVIVA
VIVCTLVAVLGATLYYFYKGKALPCGRSGKQEITLPPTRKSEFVVEVKSDKLPEEMA
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17. .1963
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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cctgaaa 1194	agagaagagacaggccaggtgctggaaagggggcctgtgcttcagttgcatgac	1135	Qy
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CAACCCT 859	GTGGGGCTGCTGAAGGAAGGGGATCATGTGACAATCAGGTGTCTGACAGATGGC	800	Db

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Taira, E., Okumura, S. and Miki, N.
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Eutheria; Rodentia;
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79.8%;
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                                                                                                                                                                                                                                                                                                                                               Score 1204.2; DB 11; Length 1988; Pred. No. 6.9e-252; D; Mismatches 358; Indels 6;
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Sciurognathi; Muridae; Murinae;
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- B .	9	GTGGAATGGTTTTGATTCACAAGGAGGAGGCAGATACCCATTTCCGTGTGCACCAG 2	5
ν			42
문	257	GCAAGGCCAGAGTGAACCTGGGGAATATGAACACCGCCTCAGCCTCCACGGCCCA	6
8 양	295 317	gctactctggccctgactcaagtcaccccccaagacgaggcgcatcttcttgtgccagggc 35 	6 4
οy	355	agcgccctcggtcccaggagtaccgcatccagctccgcgtctacaaagctccggaggag 41	4
	377	CAGCCACGGCCCCAGGATCACTATGTTCAGCTGCAAGTCTACAAGGCTCCAGAGGAG 43	6
, Q	دست ر	aaggagcctgaggaggtc 47	15
문	w	CAACTATCCAAGCCAACGTGCTGGGCATCCACGTGGACATACAAGAGCTTAAGGAGGTT 49	9
ρ γ		ggtaccccattcctcaac 	4 رن
ρy	535	ggcctctgaaggaggagaagaaccgggtccacattcagtcgtcccagactgtggagt	***
용		TTGCAAGAGGAGGAGAACCGCGTTCATATCCAGTCGTCACAGACCGTGGAGTCC 61	9
} &	595	gtattctgaaggcacagctggttaaagaagacaaagat	, 42-
Ş (ו וט	CCCSAGTTTTACTGTGAGCTCAACTACCGGCTGCTGCGAGTGGGAACCACGATGGAAGGATCACA	- (
문 *	7	GTCAGCTACCGGCCGCCCAGTGGGAACCGCATGAAGGAATCT 7	O1 4
ν	715	ggaagtcaccgtccctgttttctacccgacagaaaaagtgtggctg	444
용	737	AGGAGTCACTGTCCTGTTATACCCTGCAGAAAAAGTGTGGGTGG	07
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당 .	Ġ		6
Ωy	895	acgacaacggggtcctggtgct;	**
8	917	CCGATGAAAACGGTCTCCTGTCCTTGGAGCCCGCCCAGAAGCACCACAGTGGGGTCT	01
. Ογ	955	cgctgctgagtgaaccacaggaacta 10	14

ρ γ	1015 1037	agcccctgagagacaggaaggc 10 TGCCCCTGAAGTCCAGGAAGGT 10	74 96
γ	07	gcagoctcaccotgacotgtgaggcagagagtagccaggacotcgagttocagtggotg 11	34
용	1097	TTGAGTGGCTG 11	56
ν		agaagagacaggccaggtgctggaaagggggcctgtgcttcagttgcatgacctgaaa 11	94
	1157	AGGCCAGCTTCTGGGAAAGGGGCCCATCCTTCAGCTAAACAACGTGAAA 12	91
γ	وز	ggaggcaggaggcggctatcgctgcgtggcgtctgtgcccagcatacccggactgaac 12	54

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REFERENCE
AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                   Mus musculus mRNA for s-AB035509
AB035509.1 GI:10566954
S-gicerin/MUC18.
Mus musculus (strain:BAL
                                                                                                                                                            Direct Submission
Submitted (03-DEC-1999) to the DDBJ/EMBL/GenBank databases.
Taira, Osaka University Medical School, Department of Pharmo
2-2 Yamada-oka, Suita, Osaka 555-0871, Japan
(E-mail:etaira@pharmal.med.osaka-u.ac.jp, Tel:+81-6-6879-35:
                                                                                                                                                                                                                              mouse s-gicerin/MUC18
published Only in DataBase (2000)
2 (bases 1 to 2772)
Taira, E., Okumura, S. and Miki, N.
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 2772)
Taira, E., Okumura, S. and Miki, N.
                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; M
                                                                                                                                                    Fax:+81-6-6879-3521)
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                          /gene="s-gicerin/MUC18"
20. .1840
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/gene="s-gicerin/MUC18"
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LALSHYTPPDERMFLCKSKRPRLQDHYVELLQVFKAPEEPTIQANVVGIHVDRQELREV
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VIVCTLVLLVTLTTLLPDSSQTTGLSTLTVSHTRANSTSTEKKLPQPESKGVVIVA
VIVCTLVLAVLGAALYFLYKKGKLPCGRSGKQEMERNTSI"
75 a 706 c 749 g 642 t
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2772;

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agggaagtcaccgtccctgttttctacccgacagaaaaagtgtggctggaagtggaagccc
                                                                                             gcccagttttactgtgagctcaactaccggctgcccagtgggaaccacatgaaggagtcc
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pred. No. 1.6e-250;
0; Mismatches 362;
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Submitted (15-OCT-1996) D. Dunon,
Unite CNRS 1135, Equipe Adhesion (
Bernard, 75005 Paris, FRANCE
Bernard, 5005 Paris, FRANCE
Related sequences: D3859 and D496
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QWRDAGRRKVAEGNQLLTTLTFETSSNFSCTWKARSVPGLEQSKOVAVAKKKRPRIV
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/strain="H.B19ov+"
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gicerin,	ression and functional analysis of a novel isoform of immunoglobulin superfamily cell adhesion molecule Biol. Chem. 270 (48), 28681-28687 (1995) 81930	TITLE JOURNAL MEDLINE	
о,С.Н.,	1 to 2584) Nagino,T., Taniura,H., Takaha,N., Kim,C.H., Kiiguchi,H. and Miki,N.	REFERENCE AUTHORS	_
2-21,	<pre>ka University School of Medicine, Pharmacology; Suita, Osaka 565, Japan aira@pharmal.med.osaka-u.ac.jp, Tel:81-6-879-35 79-3529)</pre>		
CO.	ion MAR-1995) to the DDBJ/EMBL/GenBank database	TITLE JOURNAL	
7es;	Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Avenognathae; Galliformes; Phasianidae; Phasianinae; Gallus 1 (bases 1 to 2584)	REFERENCE	
•	(strain:Leghorn) adult gizzard cDNA t da gtll.	SOURCE ORGANISM	
ılin	008910 ursor; cell adhension molecule; immunoglobu	VERSION KEYWORDS	
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yt 1733 1873	ggcgttggtcatcgttggctgtgattgtgtgcatccttggtccttggcggtgctgggcgctg 	Qy 1674 g Db 1814 A	
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a 1553	tycacygcctccaacyacctgygcaaaaacaccagcatcctctcctygagctggtca	0у 1494 а	_
T 1738	CACATEGACETER LT	Db 1679 G	
a 143	cygcccacatctcctygaacytcaacygcaacytgaacaagaccaagatccac	137	
C 1621	CCGCTGTACGTGCGGCAGGACGAAGTGATCAACCTGACCTGCAAGGCCATCGCCTTCC	Db 1562 C	_
c 1373	gaaggtgtgggtgaaagagaatatggtgttgaatctgtcttgtgaagcgtcagggcaccc	Qy 1314 (_

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tccacattcagtcgtcccagactgtggagtcgagtggtttgtacaccttgcagagtattc
                                                                               ccattcctcaagtcatctggtacaagaatggccggcctctgaaggaggaggagaaccggg
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                                                           CGTCCCCCAACATCACCTGGTACAAGAACGGGGAGCCGCTGCTGCAGGAGGAGGACAAGA
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milarity 50.6%;
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VKEGDDVKLVCDADGNPAPVFSFFRRELGDSWQDMTSLADTNDGVLMLHNVSKSSGL
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VKEGDDVKLVARGEGDVLLTNLTFETSSNEFSCRVKARSVPGLEGSKQVAVAVKKGRPIL
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RAGAMCRVSNALGVSEKHIQLLDQKPSESKGIIIVAIIVCILVVAVLGSIIYFLHKKG
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/strain="Leghorn"
/db_xref="taxon:9031"
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/protein_id="BAA08648.1"
/db_xref="GI:1008911"
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/dev_stage="adult"
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2131	CAAAAGCCATCGGAGAGCAAAGGCATCATCGTGGC	2089	D D
1693	gcacctccacagagagaaagctgccggagcccggagagccgggggggg	1634	Qy
2088		2089	DЪ
1633	agagccaa	1574	Qy
2088	G	2057	Db -
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1939	10	1880	Db
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1819	TCAGCTGCAGAGTGAAGGCTCGCAGTGTGCCGGGGCTGGAGCAGCAAGCA	1760	Db .
1273	ctycgtggcytctytycccaycatacccggactgaaccgcacacagctggt	1214	Qy
1759	AGGTGGCAGAAGCAACCAGCTCCTGCTGACCAACCTTCGAGACCTCCAGCAACT	700	ם מם
1213)ggggcctgtgcttcagttgcatgacctgaaacgggaggcaggagg	1154	Qy
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913	gtc	854	Qγ
1402	CAG	1343	Db
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1222		63	Db
682	gcacagctggttaaagaagacaaagatgcccagttttactgtgagctcaact	623	Qy
1162	CAAAGATCCTGACCACGTTGGTCCGCGAGTCGAACGGGCTGTACACGGTGGTGAGCACTC	1103	Db

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REFERENCE
AUTHORS
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Sers,C., Kirsch,K., Rothbacher,U., Riethmuller,G. and Johnson,J.P.
Genomic organization of the melanoma-associated glycoprotein MUC18:
Implications for the evolution of the immunoglobulin domains
Proc. Natl. Acad. Sci. U.S.A. 90 (18), 8514-8518 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H.sapiens MUC18 gen
X68267
X68267.1 GI:602337
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1 (bases 1 to 2015)
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superfamily; melanoma associated protein.
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                                                                                                                                                                                                   Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924) On May 31, 2000 this sequence version replaced gi:6997762.
                                                                                                                                                                                                                                           Submitted (05-JAN-2000) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                                                                                                                           Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                      Published Only in DataBase (2000) In press 2 (bases 1 to 173038)
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            Assembly program: Phrap; version 0.990329
Consensus quality: 149676 bases at least 040
Consensus quality: 160868 bases at least 030
Consensus quality: 167161 bases at least 020
                                                                Web site: http://hgp.gsc.riken.go.jp/Contact: hattori@gsc.riken.go.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence updated (26-May-2000)
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32322	CGTCTGTGCCCAGCATACCCGGCCTGAACCGCACACAGCTGGTCAACGTGGCCAT	32381	Db
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1224	ameetataettenaattaenataaeetaaanaaaaanaaaaaaaa		Ş
32442	TGCTCTTTCCCAGACCCTCTGACCCATCTCTCATCCCAGACAGGCCAGGTGCTGGAAAGG	32501	Db
1164	gacaggccaggtgctggaaag	1142	Qy
32502	CCAGGCGGGTCTGGGGGCAAGGGGCTGATGGGGTGGGGT	32561	Db
1141		1142	Оу
32562	GACCTGTGA-GCAGAGAGTAGCCAGGAGCTCGAGTTCCAGAGGCTGAGAGAA	32620	Ф
1141	tgacctgtgaggcagagagtagccaggacctcgagttccagtggctgagagaag	1088	Qy
32621	TCTGACGTCCGAGTGAGTCCCGCAGCCCCTGAGAGACAGGAAGGCAGCAGCCTCA-	32679	рь
1087	tgtctgacgtccgagtgagtcccgcagcccctgagagacaggaaggcagcagcctcaccc	1028	Qy
32680		32739	Db
1027	atg	1025	Qy
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1024	cacaggaactactggtg	1003	Qy
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942	aggaagagacaaccaacgacaacggggtcctggtgctggagcctgccggaaggaa	883	Qy
32920	CGGGAGGTGCACTCTGCTCACCTCCCAATCCTCCCTAGAACCCCAGCACCAGGGAGGCA	32979	Db

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201. .305
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1. .1988
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/strain="H.B190v+"
/db_xref="taxon:9031"
/dev_stage="E13"
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DEFINITION ACCESSION VERSION

Y08854.1

GI:1621231

GGHEMCAMS 2075 bp mrNA G.9allus mrNA for HEMCAM, soluble Y08854

form

RES GGH	DЬ	Qy -	Db j	Qy	Оy	9	. Q	рb	Qy	Db	Qy	ЪЬ	Qy	DЬ	Qy	Db	Qy	Db	Qy	Вb	Qy	Db	Qy	Db -	9	B	Qγ	Db _	Qy	B .	0 V	Db
RESULT 1: GGHEMCAMS LOÇUS	1739	1494	1679	1434	1374 1622	Ü	ı w	1502	1254	1442	1194	1382	1134	1325	1074	1265	1014	1205	954	1145	894	1085	840	1025	780	965	723	905	663		0	785
3 GGHEMCAMS	GTGCCGGGTGTCCA	atgcacggcctcc	GCACATGGCCAGCAACCTGA	cgagtcc	ccagcccaccatct	CLGI	aaggtgtgggt	66	ccgcacacagctgg	CTTCGAGACCTCCAGC	acgggaggcaggag	GAGGGACGCGAGGC	gagagaagagacag	GACAGCGTGAGGCTGCACTGCCCACAGCCCCGTCAAGCTGGACT	cagcagcctcaccc	GGTGAACTACATCO	actggtgaactatg	CAGGTGCCAGACAC	tgaatgtcagggc	GGATACCAACGATGO	aaccaacgacaacg		acacttcagcatc-	0	tgctgaag	GAACGTCACTGTGT	tccct	CCACTGCACCGTGC	12	GTACACGGTGGTGAGCACTCTGTTCAGCAAGGTGACACGGGAGGACCGCAACTCCCTCTT	gtacaccttgcaga	GCTGCAGGAGGAGGACAAGACAAAGATCCTGACCACGTTGGTCCGCGAGTCGAACGGGCT
2075 bp	TGTCCAACGCGCTGGG		ACCTGACGGTGC	accctgaatgtcct	CCATCTCCACTGGAGCATCAAC	GCGGCAGGACGAA	aagagaata 	reccerecr	tggtcaacgtggcca	AACTT	geggeta	GCAGGAAGGTG	gccaggtgctg	TGAGCTGCACT	tgacctgtgag	 AAGGGGTCCAG	tgtctgacg	TGGACTTGGAC	tggacttggac	GAGTCCTGATGCTGCA	gggtcctggtg	AGGAG	agca	GGGATGATGTG	gtg	THE THE THE THE TENT	tetaceegaca	ACTACTGGCTG	tcaactaccggctg	GCACTCTGTTC	gtattctgaag	ACAAGACAAAG!
mRNA	1762	1517		gtgaccccgg	ggcacggca GGGACG	ATCAACCI	= 6	TGAAGGGGAAG	atttttggccccc	CAGCTGCAGAGTGAAGG	tgcgtggcgtctg	AGGGACGCGAGGGCAGGAAGGTGGCAGAAGGCAACCAGCTCCTCCTGACCAACCTCA	gaaagggggcctg	GCCCACAGCCCCG	gcagagagtagcc	a	tccgagtgagtcccg	AGGTGCCAGACACTGGACTTGGACGATATGACGCAGCACGAAGGGGATGTGGAGCTGGT	accatgatatcgc	CAATGTC	geetgee	eeeee	gaacc	AGTTGGTCTG	aaatcaggtg	AGCACGTGGAG	aaaagtgtgg	I II \GGGACAGATG	cagtgggaac	11 11 AGCAAGGTGACAC	rcacagetggtta	ATCCTGACCACGT
VRT			ACCTGCTGCGGGCAGG	agctgttggagaca	agtgaacaagaccaag 	Ġ	<u>1</u> - 9	3CGCÁTCGTGGC	ttggatggcatt 	AGGCTCGCAGTGTGCCG	tgcccagcatacc	AGCTCCTCCTGAC	tgcttcagttgca	TCAAGCTGGACTA	aggacctcgagtt	CGTCCTCACCCCT	cccgcagcccctgagagacaggaag	 ACGAAGGGGATGT	tatcgctgctgagtgaacc		ctgcccggaaggaacacagtg	TATG	gcaga		ď	GCGCGT	ggaagtggag	CGCACCAAGGACTCTCCGCGGGT	acatgaaggagtc	GGAGGACCGCAA	aggagacaaaga	TGGTCCGCGAGTC
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Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves
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Unite CNRS 1135, Equipe Adhesion (
Bernard, 75005 paris, FRANCE
Related sequence: D38559.
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LeveIgstarlecsfsIfgwasftsIewfyvnnrplerageavehhasgyridetesse

RLSVGEDKALSISKVTRODNARTEICOWGABSOGVGESRTELVTYKIPAPPEITPNSA

GIPAQSNDMLKIAQCTSENSFPSPNITWYKNGEPLLQEEDKTKILTTLVRESNGLYTV

VSTLFSKVTREDRNSLFHCTVHYWLQGGWRTKDSPNVTVFYFDTEHVELRVARNAGI

VKEGDDVKLUCDADGWPAPVESFFRELGDSWGDMTSLADTNDGVLMLHWVSKSSGGI

VKEGDDVKLUCDADGWPAPVESFFRELGDSWGDMTSLADTNDGVLMLHWVSKSSGGL

YRCQTLDLDDMTQHEGDVELVVNYIEGVQVKMEPSSPLHEGDSVRLSCTAHSPVKLDY

QWRDARGGKVAEGNQLLLTNLTFETSSKHSINGTVRAGRVLMAALGWGAVRGC"

AISAPLYVRQDEVINLTCKAIAFPQPSFHWSINGTVRAGRVLMAALGWGAVRGC"
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/strain="H.B19ov+"
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Chicken mRNA
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D3859.1 GI:1009246

s-gicerin precursor; cell adhesion molecule; extracellular matr protein; neurite outgrowth factor-binding; laminin family; immunoglobulin superfamily; integral membrane glycoprotein.
                                                                             On Oct 6,
Sequence
                                                                                                             an immunc
J. Biol.
96081930
                                                                                                                         Taira,E., Nagino,T., Taniura,H., Takaha,N., K. Li,B.S., Higuchi,H. and Miki,N. Expression and functional analysis of a novel an immunoglobulin superfamily cell adhesion modulation. Chem. 270 (48), 28681-28687 (1995)
                                                                                                                                                                                                                                    Taira,E., Takaha,N., Taniura,H., I
Molecular cloning and functional (
cell adhesion molecule that binds
Neuron_12 (4), 861-872 (1994)
                                                                                                                                                                                                                                                                                                                                                Submitted (20-OCT-1994) to the DDBJ/EMBL/GenBank database Taira, Osaka University School of Medicine, Pharmacology; Yamadaoka, Suita, Osaka 565, Japan
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Gallus gallus
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                                                                            6, 1995 this sequence version replaced gi:559700 se updated (05-Oct-1995) by:Eiichi Taira.
/organism="Gallus gallus"
/strain="Leghorn"
/db_xref="taxon:9031"
                                                             Location/Qualifiers
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Homo sapiens chromosome 11 c.
DRAFT SEQUENCE, in unordered
                                                         AP001557
AP001557.2 GI:8117391
                               Omo
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                            HTGS_PHASE1; HTGS_DRAFT.
sapiens DNA, clone:RP11-680A7.
                sapiens
 Metazoa; Chordata;
                                                                                             clone RP11-680A7
                                                                                    pieces
   Craniata;
Vertebrata;
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 Euteleostomi;
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Direct Submission
Submitted (29-MAR-2000) to the DDBJ/EMBL/GenBank databases.
Submitted (29-MAR-2000) to the DDBJ/EMBL/GenBank databases.
Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 (Ritasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
On May 30, 2000 this sequence version replaced gi:7380892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 177595)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P. Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 177,595 genomic DNA of 11q23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hattori, M., Ishii, K., Toyoda, A., Fujiyama, A., Yada, T., Totoki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Only in DataBase (2000) In press (bases 1 to 177595)
Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 152340 bases at least Q30 Consensus quality: 165308 bases at least Q30 Consensus quality: 171688 bases at least Q20 Insert size: 174695; sum-of-contigs Quality coverage: 4.19x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                             Center project name: HumDraft11
Center clone name: RP11-680A7
----- Summary Statistics
                                                                                                                                                                                                                                                                                        Sequencing vector: PCR products; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: RIKEN Genomic Sciences Center(GSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Project Information
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NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be 223368
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201066
9187
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This record will be updated with the finished sequence as soon as it is available and the accession number will
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Search completed: March 26, 2001, 07:38:41 Job time: 6042 sec

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metastasis; treatment; detection; diagnostic test; ds.
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CC This MUC18 (humWC18) cDNA sequence is different from the humWC18 cDNA CC given in Genebank accession number N28882, Z20931. The deduced amino acid C residues from this cDNA are very different from that published by CC Johnson's group in 1989.

CC The presence of this glycoprotein has been correlated with normal vascular CC tissue, and on the smooth muscle of venules, and it expresses

CC Sporadically on capillary epithelium.

CC The method can be used as a diagnostic test for prostate cancer which has a relatively high potential for metastasis or which has metastasized.

CC This allows the physician to choose appropriate surgical, radiation, cor chemotherapeutic treatment regimens. In addition, antibody specific CC MUC18 can be used to prevent metastasis of prostate Cancer Cells.
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                               Johnson's sequence was to see the inventors. By the inventors. The presence of this glycoprotein has been correlated with melanomas to metastasize. MUC18 is also associated with nor melanomas to metastasize of venules, and it express.
  melanomas to metastasize. MUC18 is also asso
tissue, and on the smooth muscle of venules,
sporadically on capillary epithelium.
The method can be used as a diagnostic test
has a relatively high potential for metastas
The physician can then choose the appropriat
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                                                                                                s is the previously published nucleotide sequence of the Human MUC18 I adhesion glycoprotein, which is expressed on the surface of anoma cells, and can be used as a marker for prostate cancer. I sucleotide sequence is virtually identical to the humUc18 sequence forth in the invention, except for seven amino acid residues (which be due to allelic differences). However the amino acid sequence of
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    21-APR-1994;
                                                                                        W09424160-A.
                                                                                                                                                                                                                                                                                                   hypertension;
                                                                                                                                                                                                                                                                                                                           Primer; PCR; replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctgagcaccctgaatgtcctcgtgaccccggagctgttggagacaggtgttgaatgcacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       accatctcctggaacgtcaacggcacggcaagtgaacaagaccaagatccacagcgagtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atgggcctcctgcagggcagcagcggtgacaagagggctccgggagaccagggagagaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttcctctataagaagggcaagctgccgtgcaggcgctcagggaagcaggagatcacgctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtcatcgtggctgtgattgtgtgcatcctggtcctggcggtgctgggcgctgtcctctat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        accagagccaaccagcacctccacagagagaaagctgccggagccggagagccgggggcgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acceteacaceagaetecaacaceacetggeeteageaettecaetgeeagteeteat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcctccaacgacctgggcaaaaacaccagcatcctcttcctggagctggtcaatttaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atgggcctcctgcagggcagcagcggtgacaagagggctccgggagaccagggagagaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gtcatcgtggctgtgattgtgcatcctggtcctggcggtgctgggcgctgtcctctat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   accagagccaacagcacctccacagagagaaagctgccggagccggagagccgggggcgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              accetcaccagactecaaccaccactggcetcagcacttccactgccagtectcat
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                                                                                                                                                                                                                                                          mulatta
                                                                                                                                                                                                                                                                                                                                                                                              Erythropoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                             amplify; human; """
stimulation; erythrocyte;
seizure; headache; nause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   taagaagggcaagctgccgtgcaggcgctcagggaagcaggagatcacgctg
    94WO-US04361
                                                                                                                                      /product=
                                                                                                                                                                                                                                                                                                                                                human; mouse; erythropoietin;
                                                                                                                                                                                                                                                                                                                                                                                              CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189
                                                                                                                                                              Ø
                                                                                                                                      Erythropoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                     nausea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1948
                                                                                                                                                                                                                                                                                                                        proliferation
                                                                                                                                                                                                                                                                                                                                                   EP;
                                                                                                                                                                                                                                                                                                                           EP; mutein;
;cell cultu
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N50348/c
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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in Q72942-46 represent erythropoietin amplification fragments derived from mammalian DNA from renal-derived cell lines, using the primers ATG and NCO1, see Q72931 and Q99999. These sequences were used in the design of EP muteins which contain a modification, pref. a replacement of an amino acid. The EP muteins may be used to stimulate the production of erythrocytes and induce proliferation of cell cultures responsive to EP. These muteins can be used effectively at lower dosage than wild-type EP. This may reduce their potential adverse effects associated with administration of EP, such as exacerbation of hyper-
                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erythropoietin mutein(s) with increased activity and reduced adverse effects - used to stimulate erythrocyte prodn. and induce proliferation of erythropoietin-responsive cell
                                                                                                                               Monkey.
                                                                                                                                                                    disorder;
                                                                                                                                                                                   Erythropoietin;
                                                                                                                                                                                                                        Monkey
                                                                                                                                                                                                                                                               01-JAN-1980
                                                                                                                                                                                                                                                                                                   N50348
                                                                                                                                                                                                                                                                                                                                    N50348 standard; cDNA; 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 681 BP; 133 A; 233 C; 183 G; 132 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 4; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cultures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boissel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1993;
                   WO8502610-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tension, seizures , headache and nausea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BGHM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         468
                                                                                                                                                                                                                                                                                                                                                                                                                                   288
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCTGAGAGCAGGGCCAGGCCCTGCCAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                catacccggactgaaccgcacacagctggtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gttgcatgacctgaaacgggaggcaggaggcggctatcgctgcgtggcgtctgtgcccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGATGGTTCGGAGTGGAGCCGAGGCCGCATCTGGGAGGAGATGGCTTCCTGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGCAGGGGCTCGAAAGGCTGGGAAGAGTTGGCCAACACGGCCTGGCCCCGCAGGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGCGCCCGAAGCAGAGTGGTGATGCTGCGAAGGCCACTGATGGCTTTATCCATGTGCA
                                                                                                                                                                                                                        erythropoletin cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BRIGHAM & WOMENS HOSPITAL
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                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                     red
                                                      Location/Qualifiers
140..718
/*tag= a
                                                                                                                                                                                     plood
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                                                                                                                                                                                     cell; erythrocyte;
                                                                                                                                                                                                                                                                                                                                      ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44.6; Di
Pred. No. 0.06
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                 258
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.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104;
                                                                                                                                                                                     anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     681;
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                                                                                                                                                                                                                                                                                                                                                                                          RESULT
V30955/c
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   밁
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Best Local Similarity
Matches 107; Conserv
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13-DEC-1983;
21-FEB-1984;
28-SEP-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                blood cell formation and is used
blood disorders such as anaemia.
using recombinant DNA techniques
                                                                                          CDS
                                                                                                                                                                                                       expression;
                                                                                                                                                                                                                                                                                                                                                                       V30955 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1239
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mat_peptide
                                  sig_peptide
                                                                                                                                                Primates.
                                                                                                                                                                                                                                                             Monkey
                                                                                                                                                                                                                                                                                                   11-SEP-1998
                                                                                                                                                                                                                                                                                                                                        V30955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1344 BP; 280 A; 408 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  obtained from plasma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monkey erythropoietin encoded by this sequence is essential for red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 38; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KIRI-) KIRIN-AMGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\sf w} polypeptide having properties of erythropoietin - is cultivation of transformed eucaryotic or procaryotic {\sf l}
                                                                                                                                                                                                                                                                                                                                                                                                            6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTCTGAGAGCAGGCCCAGGCCCTGCCAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGCGCCCGAAGCAGAGTGGTGATGCTGCGAAGGCCACTGATGGCTTTATCCATGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgagttccagtggctgagagagagacaggccaggtgctggaaagggggcctgtgcttca 1178
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DB; P50301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGCAGGGGCTCGAAAGGCTGGGAAGAGTTGGCCAACACGGCCTGGCCCCGCAGGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gttgcatgacctgaaacgggaggcaggaggcggctatcgctgcgtggcgtctgtgcccag 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catacccggactgaaccgcacacagctggtc
                                                                                                                                                                                                                        erythropoietin;
                                                                                                                                                                                                                                                             erythropoietin
                                                                                                                                                                                                        CHO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                 (first
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83US-0561024.
84US-0582185.
84US-0655841.
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 /*tag= b
121..715
                              /*tag= a
/product=
140..220
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                                                                                          Location/Qualifiers 140..718
                                                                                                                                                                                                        chinese
                                                                                                                                                                                                                                                                                                                                                                         cDNA;
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                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.3%;
                                                                                                                                                                                                                                                             encoding cDNA
                                                                                                                                                                                                 EPO; bone marrow; reticulocyte; red bidse hamster ovary cell; diagnosis; blood
                                                                                                                                                                                                                                                                                                                                                                         1344
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                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 G; 256 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for the diagnosis and treatment of Large amounts of EPO may be obtained in contrast to small amounts See also N50345-47, N50349-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407
                                                                                                                                                                                                                          reticulocyte; red blood cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104;
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Indels

Gaps

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disorder;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 107; Conserv
           Chimeric
Chimeric
                                                       Polynucleotide delivery; plasmid CMV-KM-cmEPO; vector; gene therapy; vaccine; polycationic agent; cynomolgus erythropoietin; EPO; anaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                       1119
                                                                                                                                                                                                                                                                                                                                                                                                                      1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes monkey erythropoietin (EPO), from an example of the present invention. The present invention describes recombinant human EPO which causes bone marrow cells to increase production of reticulocytes or red blood cells, where the polypeptide is the product of expression in CHO (Chinese hamster ovary) cells of an exogenous DNA sequence encoding human EPO. EPO is potentially useful in the diagnosis and treatment of blood disorders characterised by low or defective red blood cell production.
                                 Chimeric -
                                                                                                                                                                                                                                                                      1239
                                                                                                                                                                                                                                                                                                                       1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lin
                                                                                                        Vector plasmid CMV-KM-cmEPO.
                                                                                                                                 17-AUG-1998
                                                                                                                                                           V21685;
                                                                                                                                                                                  V21685 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1344 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant human erythropoietin - potentially useful for diagnosis and treatment of blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-261957/24.
P-PSDB; W58399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU688723-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KIRI ) KIRIN AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-1998
                                                                                                                                                                                                                                               437
                                                                                                                                                                                                                                                                                              497
                                                                                                                                                                                                                                                                                                                                               557
                                                                                                                                                                                                                                                                                                                                                                                               617
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                                                                                                                                                                                                                                                                                                                                                                                                            tgagagacaggaaggcagcctcaccctgacctgtgaggcagagagtagccaggacct 1118
                                                                                                                                                                                                                                                                                                          CTTCTGAGAGCAGGGCCAGGCCCTGCCAGAC
                                                                                                                                                                                                                                                                     catacccggactgaaccgcacacagctggtc 1269
                                                                                                                                                                                                                                                                                                                                            CCAGCGCCCGAAGCAGAGTGGTGATGCTGCGAAGGCCACTGATGGCTTTATCCATGTGCA
                                                                                                                                                                                                                                                                                                                                                                 cgagttccagtggctgagagaagagacaggccaggtgctggaaagggggcctgtgcttca 1178
                                                                                                                                                                                                                                                                                              GCTGCAGGGGCTCGAAAGGCTGGGAAGAGTTGGCCAACACGGCCTGGCCCCGCAGGACAG
                                                                                                                                                                                                                                                                                                                                                                                              3; Page 34-36; 100pp; English.
                                    Macaca cynomolgus
           Bos taurus
                       Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97AU-0046867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97AU-0046867.
                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 A; 408 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.3%; 50.7%;
                                                                                                                                                                                 5107
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                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44.6; DB Pred. No. 0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 G;
                                                                                                                                                                                                                                              407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19;
                                                                    cynomolgus monkey;
                                                                                                                                                                                                                                                                                                                                                                                                                                             104;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Query Match Best Local S Matches 107

Local Similarity les 107; Conserv

Conservative

0;

2.3%;

Score 44.6; Di Pred. No. 0.13 0; Mismatches

13; DB 104; 19;

Length 5107; Indels

0;

Gaps

0,

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the polyA site of the bovine growth hormone gene. Haematocrit levels increased in SCID mice injected with the vector i.m. pcMv-KM-cmEPO is an example of a vector that can be used in novel compositions and methods for improved polynucleotide delivery into cells. In these methods, polycationic agents are used to increase the feature of the composition of the compositions are methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                            or a vaccinating viral or cancer antigen, (antisense or ribozyme). The methods and in the gene therapy of many diseases.
                                                                                                                                                                                          the frequency of uptake of a nucleic acid (see also V21683-86) into a cell. The polycationic agent can condense with the nucleic acid and inhibit serum and/or nuclease degradation of the nucleic acid. The nucleic acid can be a vector, may express a therapeutic protein or a vaccinating viral or cancer antigen, or is itself therapeutic (antisense or ribozyme). The methods and compositions can be used in the case of the case 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the human cytomegalovirus immediate early gene promoter/enhancer the polyA site of the bovine growth hormone gene. Haematocrit levels increased in SCID mice injected with the vector i.m.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polycationic agents based on alpha-amino acids, able to complex with nucleic acid - to facilitate its entry into cell, condense and protect it against serum degradation, particularly for use i
Sequence 5107 BP; 1145 A; 1463 C; 1335 G; 1164 T; 0 other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mammalian expression vector CMVKm2 (see V21684) under control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector in which cynomolgus monkey erythropoietin (EPO) cDNA (ATCC 67545) is inserted into the XbaI and BamHI sites of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This polynucleotide sequence comprises plasmid CMV-KM-cmEPO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Page 81-83; 100pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-159296/14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1996;
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                             29-JUN-2000
                                                        A10594
                                                                                 A10594 standard;
encoding a subunit of cellulose synthase.
                                                                                                                                                      CTTCTGAGAGCAGGCCCAGGCCCTGCCAGAC 1977
                                                                                                                                                                                                                             gttgcatgacctgaaacgggaggcaggaggcggctatcgctgcgtggcgtctgtgcccag 1238
                                                                                                                                                                                                                                                                   CCAGCGCCCGAAGCAGAGTGGTGATGCTGCGAAGGCCACTGATGGCTTTATCCATGTGCA
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                                                                                                                                                                               catacccggactgaaccgcacacagctggtc
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                             (first entry)
                                                                                   DNA; 10732
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Query Match
Best Local Sin
Matches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
 9642
                                                                                                                                        9522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-AUG-1998;
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rvagysaathrgnsrrsraasrysaavathrgasnsrsrgthrgythrysgsrthrrggg
                            acgggftcctggtgctggagcctgcccggaaggaacacagtgggc----gctatgaatg
                                                                  shargsrgysysgrsrcysyssrvagyaasrasasnmtasashvagmtgysaavavas
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DB; Y85179.
                                                                                      vaaasrhsghsrhaasrsrasaagysrasasysthrsrcysaagsrtraasraasrgash
                                                                                                                                                          gtccctgttttctacccgacagaaaaagtgtggctggaagtggagcc--cgtgggaatgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding a cellulose synthetic equipment - \mbox{\it amount} of cellulose synthesised in a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIZUNO K.
OJI PAPER CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42.8; DI
Pred. No. 0.49;
05; Mismatches
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                                                                                           Pseudomonas aeruginosa-derived elastase coding DNA - in which chromosomal DNA of P. aeruginosa is cut into inserted into E. coli vector for transformation, etc.
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                                                                       Claim 1; Fig
                                                                                                                                        P-PSDB;
                                                                                                                                                                                           26-AUG-1988;
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                                                                                                                                                                                                                                                                                                                    mat_peptide
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                                                                                                                                                                     (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa IFO 3455 strain
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                                                                                                                                                 1990-161272/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggcaggaggcggct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                        R04881.
                                                                                                                                                                                                                                                                                                                                                                                                                vaccine;
                                                  encodes a
                                                                      3; 13pp; Japanese
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363..431
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                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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                   protein with a signal peptide which is elastase. this is further cleaved to give DNA can be used to produce the protein by for use in vaccines for P. aeruginosa info
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                       fragments.
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Length

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RESULT
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Best Local
                                                                                                                                 WPI; 199
P-PSDB;
Numerous alpha IC-specific DNA clones were isolated. Characterisation of the sequence revealed the alpha IC coding sequence, the alpha IC initiation of translation sequence, and alternatively spliced region of alpha IC. Q37814 and Q37815 elements of the alpha IC protein. Q37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1733
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                                                                                    DNA encoding specific human calcium channel sub-units - identifying calcium channel agonists and antagonists and diagnosing Lambert Eaton syndrome
                                                                                                                                                                 Williams
                                                                                                                                                                                                                                                       14-AUG-1992;
                                                                                                                                                                                                                                                                                                 W09304083-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q37813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q37813 standard;
                                                                                                                                                                            Brenner R,
                                                                                                                                                                                                                       15-AUG-1991;
10-APR-1992;
                                                                                                                                                                                                                                                                             04-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  Human calcium
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1993
                                                                                                                                                                                                 (SALK ) SALK
                                                                                                                                                                                                                                                                                                                                                                                        Lambert Eaton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 46.
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                                                                                                                                 1993-093936/11.
DB; R33547.
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                                                                                                                                                                                                                                                                                                                                                                                                                      encoding the alpha
                                                                 Page 102-109;
                                                                                                                                                                            Ellis
                                                                                                                                                                                                INST BIOTECHNOLOGY IND
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                channel subunit;
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92US-0868354
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1..5904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA;
                                                                                                                                                                           SB,
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                                                                150pp; English.
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Pred. No. 0.
                                                                                                                                                                          DH,
                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                      human calcium channel subunit
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                                                                                                                                                                                                ASSOC
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.29;
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RESULT
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Best Local S
Matches 102
                                                                                                            20-FEB-1990;
30-NOV-1990;
15-AUG-1991;
31-MAY-1995;
                                                                                                                                               04-APR-1988;
04-APR-1989;
04-APR-1989;
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     DNA encoding human calcium channel alpha useful for recombinant production of the its modulators, and diagnosis of Lambert
                                                 WPI;
                                                                   Brenner R,
Williams ME;
                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                        V42681;
                                                                                                                                                                         04-APR-1994;
                                                                                                                                                                                          31-MAY-1995;
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                                                                                                                                                                                                                                                                                                           characterisation;
                                                                                                                                                                                                                                                                                                                   Alpha-1C
                                                                                                                                                                                                                                                                                                                                    DNA encoding human
                                                                                            (SIBI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    885
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                                         1998-456192/39.
DB; W63139.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gaaggagtccagggaagtcaccgtccctgttttctacccgacagaaaaagtgtggctgga
                                                                                                                                                                                                                                                                                                                                                                                                                                  ggataagagcccctaccccaac 2592
                                                                                                                                                                                                                                                                                                                                                                                                                                             ggaagagacaaccaacgacaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gaaggagaagaagaagctggccaggcccagagaagaagaacaagagttggtaga
                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cggagagtctccacccgccaccaagatcaacatggatgacctccagcccaatgaaaatga
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                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                            SIBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                   subunit;
                                                                          Ellis
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                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 1360 A; 1726 C;
                                                                                            NEUROSCIENCES INC
                                                                                                            90US-0482384.
90US-0620250.
91US-0745206.
95US-0455543.
                                                                                                                                               88US-0176899.
89US-0603751.
89WO-US01408.
                                                                                                                                                                                          95US-0455543
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                                                                                                                                                                                                                                                               Location/Qualifiers 1..5904
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                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                          SB,
                                                                                                                                                                                                                                                                                                            Lambert Eaton
                                                                                                                                                                                                                                                                                                                  human; calcium channel;
                                                                                                                                                                                                                                                                                                                                     calcium channel alpha-1C subunit
                                                                                                                                                                                                                                                                                                                                                      entry)
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                                                                                                                                                                                                                                                                                                                                                                                         5904
                                                                                                                                                                                                                                              "no
                                                                          Feldman DH,
                                                                                                                                                                                                                                             stop codon given"
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                           Syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1551 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
No.
                                                                          Harpold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۷Ι
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S3
    1B sub:unit protein - channel for screening Eaton Syndrome
                                                                                                                                                                                                                                                                                                            LES;
                                                                                                                                                                                                                                                                                                                   assay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100;
                                                                          , MM
                                                                                                                                                                                                                                                                                                           diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5904;
                                                                          McCue
                                                                                                                                                                                                                                                                                                                    detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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of

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.5
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be alternatively spliced when transcribed, giving more than one form of the protein from the same transcript, each having slightly different properties. In addition, the reactivity of the alpha i subunit with IgG molecules from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a diagnostic for the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes the alpha-1C subunit of a number channel. Calcium channels are membrane-spanning, multi-subunit proteins that allow controlled entry of calcium ions into cells. This leads to depolarisation events required for muscle contraction. The recombinant to depolarisation events required for muscle contraction. The recombinant
                           11-AUG-1993;
05-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2571
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                                                                                                                                                             16-FEB-1995
                                                                                                                                                                                                               WO9504822-A
                                                                                                                                                                                                                                                                                                                        misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                      misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human neuronal calcium channel subunit alpha 1c-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q84655 standard; DNA;
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                                                                                                         11-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lambert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      705 gaaggagtccagggaagtcaccgtccctgttttctacccgacagaaaaagtgtggctgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cggagagtctccacccgccaccaagatcaacatggatgacctccagcccaatgaaaatga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gaaggagaaagaagctggccaggactgccagcccagagaagaaacaagagttggtgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggataagagcccctaccccaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggaagagacaaccaacgacaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tggcaaccctccaccacttcagcatcagcaagcagaaccccagcaccagggaggcaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agtggagcccgtgggaatgctgaaggaaggggaccgcgtggaaatcaggtgtttggctga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eaton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  channel subunit; antagonist; agonist; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Syndrome;
                                                                                                                                                                                                                                                                                                                   /*tag= a
3904..3987
/*tag= b
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1391..1465
                           93US-0105536
93US-0149097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                            ′*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..6492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                 for alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    characterise the alpha lc coding sequence, the initiation of translation and an alternatively spliced region. Q84655 sets forth one alpha lc coding sequence (alpha lc-1) and R71003 sets out its deduced AA sequence. Q87834 and R72607 set out another splice variant, designated alpha lc-2. Q84656 encodes an alternative exon for the IV S3 transmembrane domain. Other alpha lc variants can be constructed by selecting alternative amino terminal ends in place of the ends in Q84655 and Q87834 and/or inserting the alternative exon in the appropriate location (see Q84655 T). In addition, a nt. sequence (see Q84655 T) can be deleted or inserted to produce an alternative alpha lc
                                                                                                                         Calcium
Lambert
                                                            Key
                                                                                                                                                              Human
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                                                                                                                                                                                                                                                                                                                                                       2511
                                                                                                                                                                                                                                                                                                                                                                                                     2451 gaagccggcagtggggaatccaaggaggagaagattgagctgaaatccatcacggctga
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 127-137; 285pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developing prods. for studying calcium channels, e. obtaining agonists and antagonists
                        W09504822-A
                                                                                                  HOMO
                                                                                                                                                                                       01-DEC-1995
                                                                                                                                                                                                                                         Q87834 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Numerous alpha 1c-specific cDNA clones were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding human
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                                                                                                                                                                                                                                                                                                                                                    cggagagtctccacccgccaccaagatcaacatggatgacctccagcccaatgaaaatga
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                                                                                                                                                              neuronal
                                                                                                                                    channel subunit; antagonist; agonist; diagnosis;
                                                                                                                        Eaton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B₽;
                                                                                                                         Syndrome;
                                                                                                                                                              calcium
                                                            Location/Qualifiers 226..6642
                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1481 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        calcium channel sub-unit(s) -
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                                                                                                                                                              channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1942 C;
                                                                                                                                                                                                                                         ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 1:
Pred. No. 0.64;
                                                                                                                                                              subunit alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1382 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6575;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Numerous alpha lc-specific cDNA clones were isolated in order to characterise the alpha lc coding sequence, the initiation of translation and an alternatively spliced region. 084655 sets forth one alpha lc coding sequence (alpha lc-1) and R71003 sets out its deduced AA sequence. Q87834 and R72607 set out another splice variant, designated alpha lc-2. 084656 encodes an alternative exon for the IV S3 transmembrane domain. Other alpha lc variants can be constructed by selecting alternative amino terminal ends in place of the ends in Q84655 and Q87834 and of inserting the alternative exon in the appropriate location (see Q84655 FT). In addition, a nt. sequence (see Q84655 PT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-AUG-1993;
05-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding human calcium channel sub-unit(s) -developing prods. for studying calcium channels,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-AUG-1994;
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                                                                                                                                                                                                                                                                                            2601
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6725 BP;
                                                                                                                                                X84332
 misc_difference
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                                                                                                                                                                                                                                                                                                                                                   gaaggagtccagggaagtcaccgtccctgttttctacccgacagaaaaagtgtggctgga
                                                                                                                                                                                                                                                                                           gaagccggcagtgggggaatccaaggaggagaagattgagctgaaatccatcacggctga
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                                                                                                                                                                                                                         ggaagagacaaccaacgacaac
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                                                                                                                                                standard;
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93US-0149097
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                                                                              nucleic
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                                                                                acid
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                                                           diagnosis;
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                                                                                 clone,
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                                                           infection;
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specification, and is included to maintain
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3615 /note= /*tag= "this nucleotide is represented specification, and is included C base numbering given in the specification" as a * in ti to maintain n the

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- 3630 /note= /*tag= "this nucleotide is represented specification, and is included base numbering given in the spe a nted as a * in the uded to maintain the specification" the in the
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- 3638 /*tag= /note= "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification" the
- 3642 3641 /note= /*tag= "this nucleotide i specification, ar base numbering g e is re and is given s represented d is included en in the spec nted as a * in th uded to maintain e specification" the

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- 3657 /note= /note= "this "this specification, base numbering base specification, nucleotide is nucleotide numbering given in e is represented as a * in the and is included to maintain given in the specification" and represented is included esented as a * in the specification" the the the
- 3659 /*tag=
- 3681 /*tag= /note= j "this nucleotide is represented as a * in the specification, and is included to maintain base numbering given in the specification" 'n the

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- /note= "this nucleotide is represented as a * in the specification, and is included to maintain base numbering given in the specification" * the
- 3698 3703 /*tag= /note= "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"

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- 3708 /note= /*tag= "this nucleotide is represented as a * in the specification, and is included to maintain base numbering given in the specification" 3
- 3713 /note= this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"
- /note= /*tag= "this nucleotide is represented specification, and is included 0 to a * in the maintain t

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RESULT 15 N93196 ID N93196 standard; DNA; 925 BP.	Qy 442 atcoctgtgaacagtaaggagcotgaggag 471	382 atc 385 rsh	Qy 322 ccccaagacgagcgcatcttcttgtgccagggcaagcgccctcggtcccaggagtaccgc 381 :::: :: :: :: : : : : :	264 cgagcagcgyctcagcctccaggacagaggggctactctggccct :: :::: :::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	Db 145 cssmmnrsnscanradcatrgnvrssbydstryngnctdcsrrtthrasrgnyvrsssym 204 Oy 204 gaagcggacgctcatcttccgtgtgcgccaggggccaggagcgaacctggggagta 263	Query Match 2.1%; Score 41.2; DB 20; Length 5059; Best Local Similarity 17.0%; Pred. No. 0.92; Matches 56; Conservative 123; Mismatches 149; Indels 2; Gaps 1; Qy 144 cggcctctcccagtccaaggcaacctcagccatgtcgactggttttctgtccacaagga 203	ry /note= "this nucleotide is represented as a * in the FT specification, and is included to maintain the base numbering given in the specification" FT /*tag= al	/*tag= /note= misc_difference 3860 /*tag=	misc_difference 3853 /*tag= ai /note= "this nucleotide is represented as a * in th specification, and is included to maintain misc_difference 3857 wase numbering given in the specification"	misc_difference 3841 /*tag= ah /note= "this nucleotide is represented as a * in specification, and is included to maintai	misc_difference 3827 /*tag= ag /note= "this nucleotid	/*tag= /note= misc_difference 3824 /note=	FT /note= "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"

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Best Local Similarity 46.9%;
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                       The monkey kallikrein gene is 93% homologous to that of the human genomic kallikrein gene. See also P92314, N93194, N93195, N93193, N93197, N93198, P93719, P93720, P93721, and P93722.
                                                                                                                                                                                                                                                                               Sequence 925 BP; 209 A; 281 C;
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                                                                                                                                                                                                                                                                                                                                                            Table IV; page 11; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 New recombinant kallikrein polypeptide(s) and encoding DNA useful as vasodilators and for treating male infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; P93722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin FK, Lu HS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JAN-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monkey.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monkey; kallikrein gene; vasodilator; male infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monkey recombinant kallikrein gene
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                      GGAGCCTGCCCGGAAGGAACACAGTGGGCGCCTATGAATGTCAGGGCCTGGACTTGGACAC
                                                                                                                                                                                                                                                                                                                                                      680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bmail: Robert_StrausDerg@nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies,
CDNA Library Arrayed by: The I.M.A.G.E. Consc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert St
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Clone distribution: MGC clone distribution information can
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/clone=lib="NJH_MCC_68"
/clone=lib="NJH_MCC_68"
/tissue_type="large_cell carcinoma"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 1.8 kb. Library constructed by Technologies."
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/db_xref="taxon:9606"
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Pred. No. 6.2e-153;
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National Institutes of Health, Mammalian
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/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo
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/db_xref="taxon:9606"
/clone="IMAGE:3876255"
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                                                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 495-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.G.E. Consortium (LLA
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 975)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collegu
                                                                                                                                                                                                                                                                  mRNA sequence.
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601491164F1 NIH_MGC_69 Homo
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                                  found through the I.M.A.G.E. http://image.llnl.gov Plate: LLCM668 row: o colum
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Location/Qualifiers
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             gcggctatcgctgcgtggcgtctgtgcccagcata--cccggactgaaccgcacacagct
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="lib="NHH_MGE:393607"
/clone_lib="NHH_MGC_69"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."

Technologies."
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95.8%;
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KEYWORDS
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Mammalia; Eutheria;
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Clone distribution: MGC clone distribution information can be
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/lab_host="DH10B (phage-resistant)"
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Pred. No. 4.4e-141;
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                                                                                  620;
                                                                                                                                                                                                                                                                                                                                                                                                 Clone from S. Wiemann, Molecular Genome Analysis, German Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg, sequenced by LMU (Ludwig Maximilians University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL042548 669 bp mRNA EST 29-FEB-2000 DKFZp434I2321_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I2321 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST (Blum, et al.)
Unpublished (1999)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            Genome Project.
No s1 sequence available.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Am Klopferspitz 18a D-82152 Martinsried, This is the 5' sequence of the clone ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Blum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blum, H., Bauersachs, S., Mewes, H.W.,
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Mammalia; Eutheria;
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/db_xref="taxon:9606"
/clone="DKF2p43412331"
/clone="DKF2p43412331"
/tissue_type="testis"
/dev_stage="adult"
                                                                                                                                                              /note="Vector: pSport1; Site_1: Not1; Site_197 c. 182 g 130 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                         sequencing
                                                                                                                                                                                                                                                                                                                   Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gassenhuber, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Germany
                                                                                                                                                                                                                                                                                                                                                                                         consortium
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Heubnerweg
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                                                                                                                                                                                                                                                                                 mRNA sequence.
BE275425
BE275425.1 GI:
                                                   CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. Plate: LLCM78 row: n column: 05 High quality sequence stop: 588.
                                                                                                                                                                                                                                                                                                               BE275425 679 bp
601121423F1 NIH_MGC_20
                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                             Contact: Robert Strausberg, Tel: (301) 496-1550
                                                                                                                                                                                   1 (bases 1 to 679)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                    Homo sapiens
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2988868"
/clone_lib="NIH_MGC_20"
                                                                                                                                                                                                                                                                                   GI:9150379
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BE871209 553 bp
601448791F1 NIH_MGC_65
mRNA sequence.
BE871209
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/lab_Nost="DH10B (phage-resistant)"
/note="Organ: skin: Yector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORIXhoI sites using the following 5;
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
59 a 196 c 197 g 127 t
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Pred. No. 7.2e-128;
D; Mismatches 18; 1
                             Homo sapiens
                               CDNA
                               clone IMAGE: 3852671
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High quality sequence stop: 551.
Location/Qualifiers
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Tissue Procurement: ATCC
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/clone="IMAGE:38E2671"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Si
Site_2: Sall; Cloned unidirectionally. Prin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the
Project. This entry can be seen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE813148 594 bp mRNA
RC1-BN0005-190700-017-h02 BN
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Ludwig Institute for Cancer Research
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/dev_stage="Adult"
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601474277F1 NH_MGC_68 H
mRNA sequence.
BE786166
BE786166.1 GI:10207364
                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg,
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 715)
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Plate: LLCM626 row: 1
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/organism="Homo sapiens"
/ob_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_68"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/tissue_type="large cell carcinoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; S
Site_2: Sall; Cloned unidirectionally. Pr
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                                                                                                                                                                                                                                                                                                                                   AA983120 729 bp mRNA EST 27-b ua35d07.rl Soares_mammary_gland_NbMMG Mus muscullus cDb IMAGE:1348717 5' similar to SW:MU18_HUMAN P43121 CELL GLYCOPROTEIN MUC18 PRECURSOR ;, mRNA sequence.
                                                                                                                                                               Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Ld
                                                                                                          Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                     The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                     Mammalia;
                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                 Mus musculus
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              This clone is available
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                                                                                                                                                                                                                                                                              house mouse.
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clone is available royalty-free through LLNL;
Consortium (info@image.llnl.gov) for further i
                        mouseest@watson.wustl.edu
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Rodentia;
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                      cataccagagccaacagcacctccacagagagaaagctgccggagccggagccggggc 1677
                                                                                                                                                         acggcctccaacgacctgggcaaaaacaccagcatcctcttcctggagctggtcaattta 1557
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                                                                                                                                                                                                                                                                                        acacagctggtcaacgtggccatttttggccccccttggatggcattcaaggagaggaag
     TCAAACAGAGCCCACAGCACCTCCACAGGGAAAAAGCTGGCAAAGCCAGAGAAAAGGT
                                                                                          accacceteacaccagactecaacaccactggeeteageacttecactgeeagteet 1617
                                                                                                                                    ACAGCCTCCAACTCCCTGGGCTCAAACACCACCACCATTGTTCTGAAGCTGGTCACTTTA
                                                                                                                                                                                                   GTAGTGAGCACCTTGAATGTCCTTGTGACGCCAGAGCTTCTGGAGACAGGTGCAGAGTGT 438
                                                                                                                                                                                                                                                                     CCCACCATCTCCTGGAATGTCAATGGTTCGGCAACTGAATGGAACCCAGATCCACAGACA
                                                                                                                                                                                                                                                                                                                                    GTGTGGGTGCAAGAATGCAGTGCTGAATCTGTCTTGTGAGGCTTCAGGACATCCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                        MGI:697509
Possible reversed clone: similarity on wrong Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_mammary_gland_NbMMG"
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/clone="IMAGE:1348717"
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/dev_stage="4 weeks"
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/strain="C57BL/6J"
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gactggttttctgtccacaaggagaagcggacgctcatcttccgtgtgcgccagggccag
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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390
Email: smitt@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred vio.989904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
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PCR PRimers
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Mammalia; Eutheria; Cetartiodactyla;
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/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2:
Library made from pooled tissue from day 11, 13, 1
and 30 embryos."
183 c 176 g 100 t
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/lab_host="DH10B"
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Bennett, G.A., Laegreid, W.W.
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                                                                                                                                                                                                                                                                  Contact: Douglas Melton
WashU-Harvard Pancreas EST Project
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 602)
Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D., Welton,D., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter Wylle,T., Marri,J., Cardenas,M., Gibbons,M., McCann,R., Cole,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE226518 602 bp mRNA EST 06-JUL-2000 ia21g07.y1 Mouse E10 5 12 5 Pancreas cDNA Library Mus musculus 5' similar to TR:095812 095812 CELL SURFACE GLYCOPROTEIN P1H12 PRECURSOR. ;, mRNA sequence.
                                                                                                                                                                         Email: dmelton@biohp.harvard.edu, meadows@fas.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequenci.
Washington University Genome Sequencing Center For inform
obtaining a clone please contact: Adimika Meadows
                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Other_ESTs: ia21g07.x1
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BE226518.1
                                                                                                                      (meadows@fas.harvard.edu)
Seg primer: -40RP from Gibco
High quality sequence stop: '
Location/Qualifiers
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/tissue_type="Pancreatic
/dev_stage="Embryonic day
/lab_host="DH10B"
                                        /sex="Both"
                                                   /clone_lib="Mouse
                                                      /db_xref="taxon:10090"
/clone_lib="Mouse E10
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, в.,
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 642)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
                                                                                                                                                                                                                                                                              AW611108 642 bp mRNA EST un77a02.y1 Sugano mouse kidney mkia Mus musculus IMAGE:2536874 5' similar to SW:MUI8_HUMAN P43121 GLYCOPROTEIN MUC18 PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                              EST
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Kohn,S.,
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                                                                                                                                                                                                                                    GI:7315849
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CAGTGGCTTGTACACCTTGAAGAGTGTTCTGAGTGCACGCCTAGTTAAGGAAGACAAAGA
                                                                                            9agt9gtttgtacaccttgcagagtattctgaaggcacagctggttaaagaagacaaaga
                                                                                                                                           TCTGCCCTTGCAAGAGGAGGAGAACCGAGTTCATATCCAGTCATCACAGATTGTCGAGTC
                                                                                                                                                                 ccggcctctgaaggaggagaagaaccgggtccacattcagtcgtcccagactgtggagtc 593
                                                                                                                                                                                                                 TGCTACCTGTGGGGAGAAACGGCTACCCCATTCCTCAAGTCCTATGGTACAAGAACAG
                                                                                                                                                                                                                                     cgctacctgtgtagggaaggaacgggtaccccattcctcaagtcatctggtacaagaatgg
                                                                                                                                                                                                                                                                                      ACCAACTATTCAAGCCAATGTCGTGGGCATCCATGTGGACAGGCAAGAGCTCAGGGAGGT
                                                                                                                                                                                                                                                                                                               gccaaacatccaggtcaaccccctgggcatccctgtgaacagtaaggaggctgaggaggt 473
                                                                                                                                                                                                                                                                                                                                                            CAAGCGACCACGGCTCCAGGATCACTACGTTGAGCTTCAGGTCTTCAAAGCCCCCAGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTACTCTGGCCCTGAGTCACGTCACTCCCCATGATGAGCGAATGTTCCTGTGTAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R. and Wilson, R. The WashU-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTGCAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGRECCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI show be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
/lab_host="DH10B"
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/clone_lib="Sugano mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL"
/db_xref="taxon:10090"
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79.0%;
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Pred. No. 1.4e-95;
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410; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J. Sequence identification of 2,375 human brain genes Nature 355, 632-634 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 3018699423
Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bioinformatics
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                                                                                                                      /note="vector: lambdaZAP-II; The hippocampus library (#4 above) was subtracted with a fibroblast cell line cDNA library (Stratagene cat. #936209; WI38 lung fibroblast cell line; oligo-dT + random primed cDNA synthesis; lambdaZAP-II vector, 1.0kb average insert size.) by the method of Sive & St. John (Nucl. Acids Res. 16:10937, 198; "")
                                                                                                                                                                                                                                                                                             /db_xref="ATCC (dna):78811D"
/db_xref="ATCC (inhost):78811"
/db_xref="GDB:DOS1202E"
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/clone="HHCPQ51"
                                                                                                                                                                                                                                           /clone_lib="Subtracted Hippocampus, Stratagene (cat.
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1 (bases 1 to 423)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA191148 423 bp mRNA EST 10-MAR-1998 zp86e01.rl Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627096 5' similar to SW:MUJ8_HUMAN P43121 CELL SURFACE CLYCOPROTEIN MUC18 PRECURSOR ;, mRNA sequence.
AA191148.1 GI:1779842
                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2045 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 355.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Wilson RK
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        86
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/clone="IMAGE:627096"
                                                                                                                                                 /clone_lib="Stratagene HeLa cell s3 937216"
/sex="female"
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                                                                cacagagagaaaagctgccggagccggagagccgggggcg-tggtcatcgtggctgtgattg
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                                                       CACAGAGAAAAGCTGCCGGAGCCGGAGAGCCGGGGGCGTTGGTCATCGTGGCTGTGATTG
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P81222	P81229	R39685	W83137	W06872	R54713	P93999	Y13566	Y08404	W08747	W00182	W22844	R65168	W74152	W14802	R13251	R13906	P94014	W46734	R49733	R38548	R21081	R10316	R08118	R38550	R13905	W83927	Y70469	W81030	Y59498	54	81	Y88565
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ALIGNMENTS

Y42404;

Y42404 standard; Protein; 646 AA.

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Claim 17; Page 7; 80pp; English
                                             WPI; 1999-540899/45.
N-PSDB; Z20930.
                                                                    Wu
                     expression
                         Detection of metastatic prostate cancer, by detection of MUC18
                                                                                                                                                                             prostate cancer; melanoma; cell adhesion; glycoprotein;
metastasis; treatment; detection; diagnostic test.
                                                                                                   03-MAR-1998;
                                                                                                                  02-MAR-1999;
                                                                                                                                   10-SEP-1999.
                                                                                                                                                                                                        Human MUC18
                                                                                                                                                                                                                     01-DEC-1999 (first entry)
                                                                                   (UYEM-) UNIV EMORY.
                                                                                                                                                  W09945392-A1
                                                                                                                                                                 Homo sapiens
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                    in prostate cancer cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc glycoprotein, which is expressed on the surface of melanoma cells, cc and can be used as a marker for prostate cancer.

Cc and can be used as a marker for prostate cancer.

Cc this MuCl8 (humUCl8) cDNA sequence is different from the humUCl8 cDNA cells.

Cc given in Genebank accession number N28882, Z20931. The deduced amino acid compared to the compared to the compared to the published by compared to the compared to the presence of this glycoprotein has been correlated with the ability of compared to metastasize. MUCl8 is also associated with normal vascular cusume, and on the smooth muscle of venules, and it expresses compared to the capture of the method can be used as a diagnostic test for prostate cancer which has a relatively high potential for metastasis or which has metastasized. The physician can then choose the appropriate surgical, chemotherapeutic can be used to prevent metastasis of process.
RESULT
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This sequence differs from the one proposed by the inventors, t acid sequence is 603 amino acid residues while the present sequence is 603 amino acid residues.

Z20930 has 646 
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metastasis; treatment; detection; diagnostic test.
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expression in prostate cancer cells .
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              HCAPro.1 (R97230) and HCAPro.2 (R97231) are novel human haematopoietic cell antigens associated with stem cells. They are the respective products of nucleic acid sequences HCASeq.1 (T28819) and HCASeq.2 (T28820) obtd. from human CD34+ bone marro Expression systems are provided for prodn. of recombinant HCA proteins. The proteins are useful as stem cell marker proteins functional studies, and can also be used to produce antibodies that allow the purification of stem cells from haematopoietic antibodies.
                                                                                                                                                                                                                                                                                   DNA encoding human haematopoietic cell antigen proteins stem cell marker proteins in functional studies and for
                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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Human activated leukocyte cell adhesion molecule (W06891) or ALCAM is a CD6 ligand present on the surface of thymic epithelial cells, monocytes, activated T-cells, and other cells. Its amino acid sequence was deduced from cDNA clones (T46075) obtd. from HL60 and T-cell lines. ALCAM polypeptides can be produced, e.g. as a fusion proteins, in transformed host cells. They are useful for inhibiting CD6/CD6 interactions between colls.
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                                                                                                   CD6 ligands present on surface of thymic epith develop prods. for treating e.g. inflammation, rejection or neuro:degenerative diseases
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givvglllaalvagvvywlymkksktaskhvnkdlgnmeenkkle
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/label=
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/label=
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                                                                                                                      leukocyte-cell adhesion molecule;
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This polypeptide is a human CD6 ligand (see W47088), designated activated leukocyte-cell adhesion molecule (ALCAM), that is present on the surface of thymic epithelial cells, monocytes, activated T cells and a variety of other cells. Its amino acid sequence was deduced from cDNA clones (see V13954) isolated from human T cell and HL60 cDNA libraries. It is the human homologue of chicken BEN, and shows homology to neurolin, RAGE and MUC18. Anti-CD6 ligand antibodies, or their binding fragments, are useful for inhibiting binding of CD6 present on the surface of a first cell to that present on a second cell. CD6 ligands and anti-CD6 ligand antibodies are also useful in screening test compounds for the ability to inhibit binding of CD6 ligand to an anti-CD6 ligand ability to inhibit binding of CD6 ligand to an anti-CD6 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                               Aruffo A,
Siadak AW;
                                                                                                                                                                                                                                                           Claim 3;
                                                                                                                                                                                                                                                                                            Activated leukocyte-cell adhesion molecule (ALCAM), a new CD6 useful for screening compounds which inhibit interaction of and CD6 ligand antibodies
antibody
                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-120703/11
N-PSDB; V13954.
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(all claimed).
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"encoded by AYG (polymorphism in nucleotide
sequence)"
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        (SYST-) SYSTEMIX INC
                                                      02-FEB-1995;
                                                                                                    EP716146-A2.
                               06-DEC-1994;
                                                                             12-JUN-1996
                                                                                                                         Homo sapiens
                                                                                                                                                 HCAPro.2.
                                                                                                                                                        Stem cell marker; haematopoietic cell antigen; HCA; HCASeq.2;
                                                                                                                                                                                    Stem cell marker HCAPro.2.
                                                                                                                                                                                                           08-OCT-1996
                                                                                                                                                                                                                                   R97231;
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                                                                                                                                                                                                                                                                                                                                      AVIVCILVLAVLGAVLYFLY-KKGKLPCRRSGKQEITLPPSRKSE
                                                                                                                                                                                                                                                                                                                 givvglllaalvagvvywlymkksktaskhvnkdlgnmeenkkle
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                                                                                                                                                                                                                                                                                                                                                                                                            iichvegfpkpaiqwtitgsgsvinqteespyingryys--kilispeenvt-ltctaen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         p--sfsslhyqdagnyvcetalqeveglkkresltlivegkp--qikmtkktdpsglskt
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                               94US-0352323
                                                      95EP-0300661
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Matches 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGATLALTQVTPQDERIFLCQ-GKRPRSQEYRIQLRVYKAPEEPNIQVNPLGIPVNSKEP 155
                                                                                         giavglllaalvagvvywlymkksktaskhvnkdlgnmeentkle
                                                                                                                       AVIVCILVLAVLGAVLYFLY-KKGKLPCRRSGKQEITLPPSRKSE
                                                                                                                                                                                  DLGKNTSILFLELVNLTTLTPDSNTTTGLSTSTASPHTRANSTSTERKLPEPESRGVVIV
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                  standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                         fractions and extracting mRNA from them, and differentially analysing the mRNA in comparison with control samples. The method is used to identify genes whose expression is responsive to a specific stress. The identified genes are employed in determining risk associated with a physiological or disease state. The risk determination methods are used for testing a medicament for gene therapy. These medicaments, or genes identified by the method of the invention, are used for treating, preventing or controlling a physiological or disease state (especially osteoporosis or toone density or other factors causing or contributing to osteoporosis or its symptoms or other conditions involved in mechanical stress or its lack. The methods can also be used for advancing research or studies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identification of genes responsive to a specific mechanical stress. The method comprises applying the mechanical stress to an organism (tissue or cells comprising bone cells), isolating the specific cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is obtained from a clustral X alignment with protein 608. Protein 608 was identified using the method of the invention after subjecting rat osteoblasts to mechanical stress. Expression of the 608 gene was found to be upregulated by about 3-fold in cells subjected to mechanical strain. The specification describes a method for the
 1885
                                                                                                                                       1782
                                                                                                                                                                                                         1741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identification of stress induced genes preventing, treating or controlling ost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (QUAR-) QUARK BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9960164-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mechanical stress; gene therapy; protein bone development; gi/3328186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y53667;
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1999;
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                                                                   1839
                                 204
                                                                                                     152
                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                       95
                                                                                                                                                                                                                                       35 LYEYEYGSTALLKCGLSQSQGNLSHYDWFSVHKEKRTLIFRVRQGQGQSEPGEYEQRLSL
                                                                                                SKEPEEVATCVGR-----NGYPIPQVIWYKNGRPLKEEKNRVHIQSSQTVESSGLYT
                                                                                                                                                                       QDRGATLALTQVTPQDERIFLCQGKRPR-SQEYRIQLRVYKAP--EEPNIQVNPLGIPVN
                                                                                                                                                                                                     lyeviendtitmdcgvtsrp--lpsiswfrgdk-----
                                LQSILKAQLVKEDKDAQFYCELNYRLPSGNHMKESREVTVPVFYPTEKVWLEVEPVGMLK 263
                                                                                                                                   spdgshitinkaklsdggkyicrasneagtsdidlilkilvppkidksniignplai---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 6A-R; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mor O,
-envqvtdqgrytctatnr--
                                                                                                                                                                                                                                                                           Conservative
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                                                                -vartiylecpisgipqpdviwtkngmdinmtdsrvil--aqnnetfgi--
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                                                                                                                                                                                                                                                                                           7.98;
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                                                                                                                                                                                                                                                                           84;
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                                                                                                                                                                                                                                                                                         Score 266; DB 21;
Pred. No. 8.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feinstein
                                                                                                                                                                                                                                                                             Mismatches
 -gg--kashdfsldvlsppefdihgtqpt-ikr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  608; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Faerman
                                                                                                                                                                                                                                                                                                           Length 3117;
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                                                                                                                                                                                                                                                                             Indels
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RESULT
Y08402
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                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                            Drosophila sp
                                                                                                                                                                                                                                                                                                                                                                                                                     ROBO1; ROBO2; roundabout;
cell morphology; screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y08402 standard; Protein; 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2214 rlpaqqsltlqclaqgkpvpqmr 2236
                                                             This invention describes novel Robo (roundabout) polypeptides, involved in nerve guidance which heve been isolated from Drosophila sp., c. elegans, human and murine samples. The products of the invention can be used to raise anti-Robo antibodies, which can be used to modulate cell be used to raise anti-Robo antibodies, which can be used to modulate.
                                                                                                                                                                                                                                                                                                                                                                  WO9920764-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y08402;
                                                                                                                                                                                                                      Goodman CS,
                                                                                                                                                                                                                                                                                                                20-OCT-1998;
 Sequence
                           function or morphology. The Robo polynucleotides and fragments are as probes and primers and for production of the Robo polypeptides. probes and primers are also useful in screening assays.
                                                                                                                               Claim 1; Page 52-56; 80pp; English
                                                                                                                                                         Robo
                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                              (REGC ) UNIV
                                                                                                                                                                                                                                                                         14-NOV-1997;
20-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            v-ldvftppvvsvksdnpikalgetitlfcnasgnpypqlkwakggslifdspdgarisl
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                                                                                                                                                     polypeptides, a
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                          s and prime
nd primers
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                                                                                                                                                                                                                      Kidd T,
                                                                                                                                                                                                                                                 CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROBO2
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97US-0062921
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 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      screening
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                                                                                                                                                        new immunoglobulin
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                                                                                                                                                                                                                         Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                 nerve guidance;
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                                                                                                                                                                                                                         ΚJ,
                                                                                                                                                                                                                         Tear G;
                                                                                                                                                         superfamily member
                                                                                                                                                                                                                                                                                                                                                                                                                                     human; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                     cell
                                                                                                                                                                                                                                                                                                                                                                                                                                     function;
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Query Match

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modulation; nerve
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                                                                                                                                                                                                                                                                                             30-JUL-1999
                                                                                                                                                                                                                                                                                                                     Y13564;
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 Disclosure;
                                            WPI; 1999-338008/28
N-PSDB; X55768.
                                                                              Goodman C,
                                                                                                                                               13-NOV-1998;
                                                                                                                                                                     27-MAY-1999
                                                                                                                                                                                            WO9925833-A1
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                       Modulation of Robo-Comm
                                                                                                 (REGC ) UNIV CALIFORNIA.
                                                                                                                         14-NOV-1997;
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Page 34-38;
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cell
                                                                              Mitchell
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                     polypeptide interactions
 56pp; English
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                                                                              ΚJ,
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                                                                               Russell
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Best Local Sin
Matches 119;
                                                  Polymerase chain reaction; primer; PCR; amplify; VCAM-1; ICAM1 vascular cell adhesion molecule; monoclonal antibody; chimera: VLA-4; expressing cells; intracellular adhesion molecule; VCAM-
             Synthetic
                                                                                                                                                                                                                  R39686 standard;
                                       VCAM-6D; substitution; Ig superfamily;
                                                                                                                       VCAM-6D/ICAM4-1.
                                                                                                                                                       23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (commissureless) polypeptide in contact with a cell expressing active Robo (roundabout) on its surface. The method comprises modulating the effective amount of Comm polypeptide in contact with the cell, where the amount of expressed active Robo is specifically modulated inversely with the modulation of the effective amount of Comm in contact with the cell. The method is used to modulate the amount of active Robo expressed on a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell. The method can be used to screen for agents that modulate Robo:Comm
interactions. This is particularly useful for modulating nerve cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to a method for modulating the amount of
                                                                                                                                                                                                                                                                                                                                                                                    LVNLTTLTPDSNTTTGLSTSTASPHTRANSTSTERKLPEP-ESRGVVIVAVIVCILVLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGYRCVASVPSIPGLNRTQLVNVAIFGPPWMAFKERKVWVKENMVLNLSCEASGHPRPT
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                                                                                                                                                   (first
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                                                                                                                                                                                                                Protein;
                                                                                                                                                   entry)
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23.8%;
                                                                                                                                                                                                                  647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 252; DB pred. No. 2.6e. 72; Mismatches
                                                                                                                                                                                                                  A
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2.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1381;
                                                                                  ICAM1;
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C (VCAM)/ICAM polypeptide which was used to determine regions of VCAM-1 cinvolved in recognition of VLA-4-expressing cells. Recombinant genes cenceding VCAM/ICAM (intracellular adhesion molecule) chimeras were produced by exclsing portions of the VCAM-7D and VCAM-6D cDNAs and Creplacing them with analogous regions of ICAM-1 using unique restriction endonuclease sites within the VCAM-1 cDNA, and PCR centraction continued as a site of ICAM-1 cDNA, and PCR continued fragments of ICAM-1 (see also 043578-84). Substitution of one continued contin
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 83-86; 108pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody to epitope on the fourth Ig-like domain VCAM-7D - for treating inflammation or disease associated will be undotyte binding to endothelium e.g. post-reperfusion injur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Benjamin CD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-243235/30
N-PSDB; Q46662
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Query Match Best Local Similarity

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                                      MLKEGDRVEIRCLADGNPPPHFSISKQNPSTREAEEETTNDNGVLVLEPARKEHSGRYEC
                                                                    tftpvi----edigkvlvcraklhidemdsvptvrgavkelgvyispkntvisvnpst 234
                                                                                                            TLQSILKAQLVKEDKDAQFYCELNYRLPSGNHMKESREVT--VPVFYPTEKVWLEVEPVG
                                                                                                                                                    eagkpitvk-----csvadvypfdrleidllkgdhlmksqefledadrksletkslev
                                                                                                                                                                                         --GIPVNSKEPEEVATCVGRNGYPIPQV-IWYKNGRPLKEEKNRVHIQSSQTVESSGL-Y 202
                                                                                                                                                                                                                                                                                                                                              PAPELVEVEVGSTALLKCGLSQSQGNLSHVDWFSVHKEKRTLIFRVRQGQGQSEPGEYEQ
                                                                                                                                                                                                                                                             RLSLQDRGATLALTQVTPQDERIFLCQ---GKRPRSQEYRIQLRVYKAPEEPNIQVN-PL 146
                                                                                                                                                                                                                               -----gtnstltlspvsfenehsylctvtcgh--kklekgiqvelysfpkdpeihlsgpl
                                                                                                                                                                                                                                                                                                         pgpr-iaaqigdsvmltcsvmgces--psfsw-----rtqidsplsgkvrse-----
                                                                                                                                                                                                                                                                                                                                                                                        7.3%; Score 244.5; DB 14; ilarity 21.5%; Pred. No. 3e-09; Conservative 100; Mismatches 255;
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymerase chain reaction; primer; PCR; amplify; VCAM-1; ICAM1; vascular cell adhesion molecule; monocional antibody; chimera: vascular cella difference intracellular adhesion molecule; VCAM-VCAM-6D; substitution; Ig superfamily; homology.
                                                                             Monoclonal antibody to epitope on the fourth Ig-like domain of VCAM-7D - for treating inflammation or disease associated with
                                                                                                                                                          N-PSDB; Q43588
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                                                                                                                                                                                                                                  Benjamin CD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                     (BIOJ ) BIOGEN
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                                                     endothelium
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ule; VCAM-7D;
                                                  injury,
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Disclosure; Page 56-59; 108pp; English.

encoding VCAM/ICAM (intracellular adhesion molecule) chimeras were produced by excising portions of the VCAM-TD and VCAM-6D cDNAs and replacing them with analogous regions of ICAM-1 using unique restriction endonuclease sites within the VCAM-1 cDNA, and PCR generated fragments of ICAM-1 (see also Q43578-84). Substitution of the excised VCAM-1 regions was done to eliminate as much as possible structural distortions what would accompany deletion of one compared commains of the VCAM-1 molecule. ICAM-1 was chosen as a donor because it is also a member of the Ig superfamily and has the highest degree of amino acid homology to VCAM-1 among superfamily members. The N-terminal three domian of VCAM-1 among superfamily members. The N-terminal three domian of VCAM-1 support adhesion to VLA-4, and VCAM/ICAM-1 and VCAM/ICAM-2 in which most of the first domain has been replaced by ICAM-1, do not bind to the anti-VCAM-1 monoclonal antibody (MAb), 489. Therefore the epitope which binds to 489 must be situated This sequence represents a chimeric vascular cell adhesion molecule (VCAM)/ICAM polypeptide which was used to determine regions of VCAM-1 involved in recognition of VLA-4-expressing cells. Recombinant genes domain 1.

 $\begin{smallmatrix} \mathbf{q} & \mathbf{x} & \mathbf{0} & \mathbf{0}$

Sequence 736

Вþ δÃ дb Qy Db Qy Ъ Qy DЪ Qy DЪ QΥ В δõ Дb Qy B QУ рь QУ В QΥ Query Match Best Local Similarity Matches 146; Conserv 469 448 411 138 195 112 pervelaplpswqpvgknltlrc---qveggapran-----ltvvllrgeklmksqef 161 542 499 521 399 357 366 306 306 248 272 162 ledadrksletkslevtftpviedigkvlvcraklhidemdsvptvrqavkelqvyispk 221 \mathfrak{S} PELVEV------PEGSTALLKCGLSQSQGNLSHVDWFSVHKEKRTLIFRVRQGQGQSEP ntvisvnp---stklqeggsvtmtcsseglpapeifwskkldng-----nlqhlsgna kkkaetgdtvlksidgaytirkaqlkdagvyecesknkvgsqlrsltldvqgrennkdyf 692 ---CTASNDLGKNTSILFLEL-----VNLTTLTPDS----NTTTGLSTSTASPHT----L-----NLSCEASGHPRPTISWNVNGTASEQDQDPQRVLSTLNVLVTPELLETGVE--ptiedtgkalvcqaklhiddmefepkqrqstqtlyvnva------REAGGGYRCVASV-----PSIPGLNRTQLVNVAIFGPPWMAFKERKVWVKENMV glvngssvtvsckvpsvypldrleiellkget--ileniefledtdmkslenkslemtfi 468 tlspvsfenehsylctvtcghkklekgiqvelysfprd-------VLEPARKEHSGRYEC-----QGLDLDTMISLLSEPQELLVNYVSDVRVSPAAPERQ---PTEKVWLEVEPVGML--KEGDRVEIRCLADGNPPPHFSISKQNPSTREAEEETTNDNGVL T-----VESSGLYTLQSILKAQLVKEDKDAQFYCELNYRLPSGNHMKESREVTVPVFY 247 EPNIQVNPLGIPVNSKEPEEVATCVGRNGYPIPQVIWYK---NGRPLKEEKNRVHIQSSQ 194 GEYEQRLSLQDRGATLALTQVTPQDERIFLCQGKR---------IVAVIVCILVLAVLGAVLYFLYK---KGKLPCRRSGKQEI 598 vylceginqagrsrkeveliiqvtpkdikltafpsesvkegdtviisctcgnvpetwiil leegssvnmtclsqgfpapkilws ---EGSSLTLTCEAES---SQDLEFQWLREETGQVLERGPVLQLHDLK---qekpftveispgpriaaqigdsvmltcsvmgcespsfswrtqidsplsgkvrsegtnstl tltliamrmedsgiyvcegv---nli------- RANSTSTERK Conservative 7.1%; 20.7%; 90; Score 237.5; DB 1*, Pred. No. 1.1e-08; ""smatches 251; -LPEPESRGVV -rqlpngelqplsenatltlistkmedsg -p----PRSQEYRIQLRVYKAPE 137 gknrke----veliv Indels Length -rdttvlvspssi 217; -peiemsg Gaps 365 305 85 632 541 572 447 410 356 305 271 498 398 30;

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                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                  identification of genes responsive to a specific mechanical stress. The method comprises applying the mechanical stress to an organism (tissue or cells comprising bone cells), isolating the specific cellular fractions and extracting mRNA from them, and differentially analysing the mRNA in comparison with control samples. The method is used to identify genes whose expression is responsive to a specific stress. The identified genes are employed in determining risk associated with a physiological or disease state. The risk determination methods are used for testing a method stress to the control samples.
1043
                                                                  1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is obtained from a clustral X alignment with protein 608. Protein 608 was identified using the method of the invention after subjecting rat osteoblasts to mechanical stress. Expression of the 608 gene was found to be upregulated by about 3-fold in cells subjected to mechanical strain. The specification describes a method for the
                                                                                                                                                                                                                                                                  medicament for gene therapy. These medicaments, or genes identified by the method of the invention, are used for treating, preventing or controlling a physiological or disatte (especially osteoporosis obone density or other factors causing or contributing to osteoporosis its symptoms or other conditions involved in mechanical stress or its lack. The methods can also be used for advancing research or studies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 32; Fig 6A-R; 308pp; English.
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ftnnvatlvfnkvnindsgeytckaensigtassktvfrigerglppsfarglkdie-gt 1101
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Pred. No. 1.8e-07;
8; Mismatches 231;
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                                                                                                                                                                                                                                                                                                             NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1; neurite outgrowth promoter; proliferation; nerve damage; sclerosis; impaired myelination; stroke; Parkinson's disease; memory; schizophrenia; Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
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29-APR-1999;
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                                                           ) OSTERGAARD S
) JENSEN P H.
) POULSEN F M.
                                    SOROKA V. RALETS I.
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Bock E,
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CC This sequence represents the human neural cell adhesion molecule (NCAM) CC amino acid sequence. NCAM is found in three forms, two of which are CC transmembrane forms, while the third is attached via a lipid anchor to CC the cell membrane. All three NCAM forms have an extracellular structure consisting five immunoglobulin domains (Ig domains). The Ig domains are CC consisting five immunoglobulin domains (Ig domains). The Ig domains are CC containing a peptide which binds to the NCAM Igl domain. The compound CC containing a peptide which binds to the NCAM Igl domain. The compound CC binds to NCAM Igl/Ig2 domains, and is capable of stimulating or promoting CC promoting the proliferation of NCAM presenting cells. The compound may be used in the treatment of normal, degenerated or damaged NCAM presenting CC cells. The compound may in particular be used to treat diseases of the CC central and peripheral nervous systems such as post operative nerve CC damage, traumatic nerve damage, impaired myelination of nerve fibres, CC disease, dementias, sclerosis, nerve degeneration associated with CC disease, dementias, disorders affecting the circadian clock or neurocular transmission and schizorbrania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuro-muscular transmission and schizophrenia. Conditions affecting muscles may also be treated with the compound, such as conditions associated with impaired function of neuromuscular connections
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                                                     ceasgdpipsitwrtstrnisseektldghmvvrsharvssltlksiqytdageyictas
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21.1%;
-VPSIPGLNRTQLVNVAIFGPPWMAFKERKVWVKENMVLNLSCEA
                                                                                                                 LREET--GQVLERGPV----LQLHDLKREAGGGYRCVAS 410
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Pred. No. 2.4e-08;
96; Mismatches 222;
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                                                                               contains six potential N-glycosylation sites.

Comparison of VCAM1 and VCAM1b ((006688) revealed that they are virtually identical except for one significant difference: VCAM1b contains an insertion of 276 nucleotides near the middle of the coding region. These nucleotides encode 92 additional amino acids which form an extra domain of 84 amino acids situated between the end of VCAM1 domain 3 and the beginning of VCAM1 domain 4. This identification is designated domain 3B.
      their
which
                                                                                                                                                                                                                        characteristic of a signal sequence. It is predicted that the N-terminal amino acid of the mature protein will be phenylalanine: The extracellular domain of the polypeptide is ca. 606 amino acids including the signal sequence and is followed by a hydrophobic transmembrane region of 22 amino acids. The protein possesses a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-1989;
28-APR-1989;
01-JUN-1989;
           binding of leucocytes to endothelial cells, and such binding c
be inhibited (i.e. inflammation can be treated) using an ELAM
(or fragment), antibodies which recognise MILA, ELAM ligands c
their fragments, carbohydrates which bind to ELAM and antibodi
                                                                                                                                                                                                         including the signal sequence and is followed by a transmembrane region of 22 amino acids. The protestance charged cytoplasmic tail of 19 amino acids.
                                                                         Cells expressing ELAM can be used to identify mols, which inhibit
                                                                                                                                                                                                                                                                                         The VCAM1 polypeptide characteristic of a si
                                                                                                                                                                                                                                                                                                                                                                                Endothelial cell adhesion mols. inhibition-detection of binding
                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 3 (A-D); 136pp; English.
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N-PSDB; Q06687.
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fragments, care.
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                                                               Polymerase chain reaction; primer; PCR; amplify; VCAM-1; ICAM1; vascular cell adhesion molecule; monocional antibody; chimera: 4B9; VLA-4; expressing cells; intracellular adhesion molecule; VCAM-7D; VCAM-6D; substitution; Ig superfamily; homology.
                                                                                                                                                                                                                      R38549 standard; Protein;
                                                                                                                                                                                          R38549;
                                                                                                                                     VCAM-6D
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                                                                                                                                                                                                                                                                                     gsyslveaqkskv 647
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 Location/Qualifiers 1..24
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Pred. No. 2e-08;
9; Mismatches 234;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody to epitope on the fourth Ig-like domain of VCAM-7D - for treating inflammation or disease associated with leukocyte binding to endothelium e.g. post-reperfusion injury,
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                               LLSEPQELLVNYVSDVRVSPAAPERQ-----EGSSLTLTCEAES---SQDLEFQWLREE
                                                              tcsseglpapeifwskk---ldngnlqhlsgnatltliamrmedsgiyvcegvnl---ig
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21.9%;
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В	Qy	DЬ	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy
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Search completed: March 23, 2001, 12:31:40 Job time: 63 sec

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ALIGNMENTS

A: Note: this sequence has been corrected in 120/10 A: Note: this sequence has been corrected in 120/10	RES 138 CC Noel CC S CC S	RESULT 1 138049 138049 138049 138049 138049 N;Alternate names: melanoma-associated glycoprotein MUC18 precursor C;Species: Homo saphens (man) C;Date: Ol-Mar-1996 #sequence_revision Ol-Mar-1996 #text_change 21-Jul-2000 C;Accession: 138049; A34507 C;Date: Ol-Mar-1996 #sequence_revision Ol-Mar-1996 #text_change 21-Jul-2000 C;Accession: I38049; A34507 C;Date: Ol-Mar-1996 #sequence_revision Ol-Mar-1996 #text_change 21-Jul-2000 C;Accession: I38049; A34507 R;Sets, C.; Kirsch, K.; Rothbacher, U.; Riethmuller, G.; Johnson, J.P. Proc. Natl. Acad. Sci. U.S.A. 90, 8514-8518, 1993 A;Title: Genomic organization of the melanoma-associated glycoprotein MUC18: implicat A;Accession: 138049; MUID:93391384 A;Reference number: I38049; MUID:93391384 A;Reference number: I38049; MUID:93391384 A;Reference type: DNA A;Reference this reference also contains a correction to A34507 R;Lethmann, J.M.; Riethmueller, G.; Johnson, J.P. Proc. Natl. Acad. Sci. U.S.A. 86, 9891-9895, 1989 A;Title: MUC18; a marker of tumor progression in human melanoma, shows sequence simil A;Reference number: A34507; MUID:90099368 A;Rojecule type: mRNA A;Reference number: A34507; MUID:90099368 A;Reference number: A34507; MUID:90099368 A;Reference number: A34507 A;Rojecule type: mRNA A;Reference number: A34507 A;Ref
	M H O	uery Match 98.9%; Score 3327; DB 2; Length 646; est Local Similarity 98.9%; Pred. No. 2.6e-205; atches 639; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
98.9%; Score 3327; DB 2; Length 646; llarity 98.9%; Pred. No. 2.6e-205; Conservative 3; Mismatches 4; Indels 0; Gaps	Qy Db	1 MGLPRLVCAFLLAACCCCPRVAGVPGEAEQPAPELVEVEVGSTALLKCGLSOSQGNLSHV 60
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Query Match 98.9%; Score 3327; DB 2; Length 646; Best Local Similarity 98.9%; Pred. No. 2.6e-205; Matches 639; Conservative 3; Mismatches 4; Indels 0; Gaps 1 MGLPRLVCAFILAACCCCPRVAGVPGEAEQPAPELVEVEVGSTALLKCGLSOSQGNLSHV 60	Qy Db	181 LKEEKNRVHIQSSQTVESSGLYTLQSILKAQLVKEDKDAQFYCELNYRLPSGNHMKESRE 240

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s-gicerin precursor - chicken
c:Species: Gallus gallus (chicken)
c:Species: Gallus gallus (chicken)
c:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
c:Accession: 150419
R:Taira, E: Takaha, N.; Taniura, H.; Kim, C.H.; Miki, N.
Neuron 12, 861-872, 1994
A;Title: Molecular cloning and functional expression of gicerin,
A:Reference number: 150419; MUID:94213753
A;Accession: 150419
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A; Residues: 1-584 <TAI>
A; Cross-references: GB:D38559; NID:91009246;
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                                                                                                                                                                                                                                                  ECLLHLRRVVLCQPRPLRSGEAVRHHASGVRIDETEYSERLSVGEDKA-LSISKVTRQDN
                                                                                                                                                                                                                                                                   FSVHKEKRTLIFR---VRQGQG------QSEPGEYEQRLSLQDRGATLALTQVTPQDE
                                                                                                                                                                                                                                                                                                                                                 CAFLLAACCCCPRVAGVPGEAEQPAPELVEVEVGSTALLKCGL-----SQSQGNLSHVDW
                                                                     LPSGNHMKESREVTVPVFYPTEKVWLEVEP-VGMLKEGDRVEIRCLADGNPPPHFSISKQ
                                                                                                                  SPNITWYKNGEPLLQEEDKTKILTTLVRESNGLYTVVSTLFSKVTREDRNSLFHCTVHYW
                                                                                                                                               IPQVIWYKNGRPLKEEKNRVHIQSSQTVESSGLYTLQSILKAQLVKEDKDAQFYCELNYR
                                                                                                                                                                                  ARTFICQVGADSQGVGESRTELYTYKIPAPPEITPNSAGIPAQSNDMLKIAQCTSENSFP
                                                                                                                                                                                                              -RIFLCQ--GKRPRSQEYRIQLRVYKAPEEPNIQVNPLGIPVNSKEPEEVATCVGRNGYP
               --NPSTREAEEETTNDNGVLVLEPARKEHSGRYECQGLDLDTMISLLSEPQELLVNYVSD
                                                  LQGQMRTKDSPRVNVTVFYPTEHVELRVATNAGIVKEGDDVKLVCDADGNPAPVFSFFRR
                                                                                                                                                                                                                                                                                                                    ---GAAGRP----
 25.7%;
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Pred. No. 1
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7; Mismatches 2
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C; Genetics:
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A;Map position: 19q12-19q13
C;Keywords: glycoprotein
F;1-31/Domain: signal sequence #status
F;32-628/Product: Lutheran blood group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lutheran blood group glycoprotein precursor - human
C;Species: Homo sapiens (man)
C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999
C;Accession: I38000; S51663
R;Parsons, S.F.; Mallinson, G.; Holmes, C.H.; Houlihan, J.M.; Simpson, K.L.; Mawby, V.Proc. Natl. Acad. Sci. U.S.A. 92, 5496-5500, 1995
A;Title: The Lutheran blood group glycoprotein, another member of the immunoglobulin A;Reference number: I38000; MUID:95296337
A;Accession: I38000; MUID:95296337
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A; Residues: 1-628 <RES>
A; Cross-references: EMBL: X83425;
A; Note: parts of this sequence, i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFSCRVKARSVPGLEQSKQVAVAVKGKPRIVAISAPLYVRQDEVINLTCKAIAFPQPSFH 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRV--SPAAPERQEGSSLTLTCEAESSQDLEEQWLREETGQVLERGPVLQLHDLKREAGG
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                                                                                                                                                                                                                                                                                 -VDWF-----SVHKEKRTLIFRVRQGQGQSEPGEYEQRLSLQDRGATLALTQV 106
                                                                                                                                                                                                                                                                                                                       GAPRILLIAVILIAA-----HPDAQAEVRISVPPLVEVMRGKSVILDC---TPTGTHDHY
                                                                                                                                                                                                                                                                                                                                                      GLPR-LVCAFLLAACCCCPRVAGVPGEAEQPAPELVEVEVGSTALLKCGLSQSQGNLSH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDSNTTTGLSTASPHTRANSTSTERKLPEPESRGVVIVAVIVCILVLAVLGAVLYFLY
                                                     HCAAHYSLPEGRHGRLDSPTFHLTLHYPTEHVQFWVGSPSTPAGWVREGDTVQLLCRGDG
                                                                                                                       NGNPAPKITWYRNGQRLEVPVEMNPEGYMTSRTVREASGLLSLTSTLYLRLRKDDRDASF
                                                                                                                                       NGYPIPQVIWYKNGRPLK--EEKNRVHIQSSQTV-ESSGLYTLQSILKAQLVKEDKDAQF 221
                                                                                                                                                                                       QVGDERDYVCVVRAGAAGTAEATARLNVFAKPEATEVSPNKGTLSVMEDSAQEIATCNSR
                                                                                                                                                                                                                     TPQDERIFIC--QGKRPRSQEYRIQLRVYKAPEEPNIQVNPLGIPVNSKEPEEVATCVGR
                                                                                                                                                                                                                                                       MLEWFLTDRSGARPRLASAEMQGSELQVTMHDTRGRSPP----YQLDSQGR----LVLAEA 115
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Pred. No. 6.9e
)3; Mismatches
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glycoprotein #s
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No. 6.9e-34;
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A:Title: Molecular cloning of the B-CAM cell surface glycoprotein A:Reference number: 137202; MUID:95042297
A:Accession: 137202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B-CAM protein - human
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #text_change 21-Jul-2000
C:Accession: I37202; S47272
C:Accession: I37202; S47272
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C;Genetics:
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A; Residues: 1-588 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                          B-CAM
   SPSPEYTLFR-
                                                                        YCELNYRLPSGNHMK-ESREVTVPVFYPTEKV--WL--EVEPVGMLKEGDRVEIRCLADG
                                                                                                                                NGYPIPQVIWYKNGRPLK--EEKNRVHIQSSQTV-ESSGLYTLQSILKAQLVKEDKDAQF 221
                                                                                                                                                                    QVGDERDYVCVVRAGAAGTAEATARLNVFAKPEATEVSPNKGTLSVMEDSAQEIATCNSR
                                                                                                                                                                                               TPQDERIFIC--QGKRPRSQEYRIQLRVYKAPEEPNIQVNPLGIPVNSKEPEEVATCVGR 164
                                                                                                                                                                                                                             MLEWFLTDRSGARPRLASAEMQGSELQVTMHDTRGRSPP----YQLDSQGR----LVLAEA
                                                                                                                                                                                                                                                                                     GAPRLLLLAVLLAA-----HPDAQAEVRLSVPPLVEVMRGKSVILDC---TPTGTHDHY
                         NPPPHFSISKONPSTREAEEETTNDN~-GVLVLEPARKEHSGRYECOGLDLDTMISLLSE
                                                      HCAAHYSLPEGRHGRLDSPTFHLTLHYPTEHVQFWVGSPSTPAGWVREGDTVQLLCRGDG
                                                                                                              NGNPAPKITWYRNGQRLEVPVEMNPEGYMTSRTVREASGLLSLTSTLYLPCRKDDRDASF
                                                                                                                                                                                                                                                       -VDWF-----SVHKEKRTLIFRVRQGQGQSEPGEYEQRLSLQDRGATLALTQV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WVKENMVLNLSCEASGHPRPTISWNVNGTASEQDQDPQR---VLSTLNVLVTPELLETGV
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PEQTGLLMGGASGGARGGSGGFGDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPQELLVNYVSDVRVSPAAPERQEG-----SSLTLTCEAESSQDLEFQWLREETGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPSPEYTLFR----LQDEQEEVLNVNLEGNLTLEGVTRGQSGTYGCRVEDYDAADDVQLS
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: X80026;
LQDEQEEVLNVNLEGNLTLEGVTRGQSGTYGCRVEDYDA---
                                                                                                                                                                                                                                                                                                                                                             18.0%;
29.2%;
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                                                                                                                                                                                                                                                                                                                                                            Score 606; DB 2;
Pred. No. 2.9e-31;
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                                                                                                                                                                                                                                                                                                                                                247;
                                                                                                                                                                                                                                                                                                                                                                         Length 588;
                                                                                                                                                                                                                                                                                                                                             Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.; Garin-Chesa, P.;
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A. Molecule type: protein
A. Résidues: 34-48 <TAN1>
C.Comment: This protein is uniquely and transiently expressed
C.Comment: This protein is uniquely and transiently expressed
C.Keywords: glycoprotein; transmembrane protein
F.1-33/Domain: signal sequence #status predicted <SIG>
F.34-588/Product: adhesion molecule SC1 #status predicted <ADF
F.500-523/Domain: transmembrane #status predicted <TRA>
F.500-523/Domain: transmembrane #status predicted <TRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JH0506
adhesion molecule SC1 precursor - chicken
C; Species: Gallus gallus (chicken)
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Ju1-2000
C; Accession: JH0506; PS0270
C; Accession: JH0506; PS0270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Tanaka, H.; Matsui, T.; Agata, A.; Tomura, M.; Kubota, I.; McFarland, Neuron 7, 535-545, 1991
A;Title: Molecular cloning and expression of a novel adhesion molecule, A;Reference number: JH0506; MUID:92030150
A;Accession: JH0506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: A; Accession: PS0270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-588 < TAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                  KESREVTVPVFYPTEKVWLEV-EPVGMLKEGDRVEIRCLADGNPPPH---FSISKQNPST
                                                                                                                               GRVLQPVEEVVVINLRKVEN-RSTGLFTMTSSLQYMPTKEDANAKFTCIVTYHGPSGQKT
                                                                                                                                                             GRPLK--EEKNRVHIQSSQTVESSGLYTLQSILKAQLVKEDKDAQFYCELNYRLPSGNHM
                                                                                                                                                                                                                    DDVSEEPTV-VKVFKQPSQPEILHQADFL----ETEKLKMLGECVVRDSYPEGNVTWYKN
                                                                                                                                                                                                                                                                                                             MPNGSPVFIAFRSSTKKNVQYDDVPDYKDRLSLSE-NYTLSIKNARISDEKRFVCMLVTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVCAFLLAACCCCPRVAGVPGEAEQPAPELVEVEVGSTALLKCGLSQSQGNLSHVDW-FS
                                          IQSEPVVFDVHYPTEKVTIRVLSQSSTIKEGDNVTLKCSGNGNPPPQEFLFYI-----
                                                                                                                                                                                                                                                                   RPRSQEYRIQLRVYKAPEEPNI---QVNPLGIPVNSKEPEEVATCVGRNGYPIPQVIWYKN
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ce: embryo
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26.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 509.5; DB 2;
Pred. No. 4.3e-25;
7; Mismatches 254;
                                                                                                                                                                                                                                                                                                                                                                                                       ----YTVNAVYGDTITMPCRLEVPDG-LMFGKWKYE
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R;Pourquie, O.; Corbel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, Proc. Natl. Acad. Sci. U.S.A. 89, 5261-5265, 1992
A;Title: BEN, a surface glycoprotein of the immunoglobulin superfami A;Reference number: A45254; MUID:92302224
A;Accession: A45254
A;Accession: A45254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   surface glycoprotein BEN precursor - chicken C;Species: Gallus gallus (chicken) C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change C;Accession: A45554; S19202
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A; Residues: 1-588 < POU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AP-ERQEGSSLTLTCEAESSQDLEFQWLREETGQVLERGPVLQLHDLKREAGGGYRCVAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S--EQDQDPQRVLSTLN--VLVTPELLETGVECTASNDLGKNTSILFLELVNLTTLTPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQEVEGLKKRKTLKLIVEGKP--QIKMTKKTNTNKMSKTIVCHVEGFPKPAVQWTVTGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - PGETEGIRSSDTYVMTDVRRNATGEYKCSLIDKSMM-----DATTITVHYL-DLQLTPS
                                                                                                                                     KESREVTVPVFYPTEKVWLEV-EPVGMLKEGDRVEIRCLADGNPPPH---FSISKQNPST
                                                                                                                                                                                                      GRPLK - - EEKNRVHIQSSQTVESSGLYTLQSILKAQLVKEDKDAQFYCELNYRLPSGNHM
                                                                                                                                                                                                                                                     RPRSQEYRIQLRVYKAPEEPNI--QVNPLGIPVNSKEPEEVATCVGRNGYPIPQVIWYKN 177
                                                                                                                                                                                                                                                                                            PNGSPVFIAFRSSTKKNVQYDDVPDYKDRLSLSE-NYTLSIKNARISDEKRFVCMLVTE
                                                                                                                                                                                                                                                                                                                          VHKEKRTLI-FR--VRQGQGQSEPGEYEQRLSLQDRGATLALTQVTPQDERIFLCQ--GK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTVTSLNVSAISIPEYDEPEDR-NDDNSEK----VNDQAKLIVGIVVGLLLVALVAGVVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTTTGLSTSTAS-----PHTRANSTSTERKLPEPESRGVVIVAVIVCILVLAVLGAVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLINKTEETKYVNGKFSSKIIIAPEENVT-LTCIAENEL--
GEVTKQIGEALPVSCTISSSRNATVFWIKDNTR--MKTSP--SFSSLQYQDAGNYICETT
                           AP-ERQEGSSLTLTCEAESSQDLEFQWLREETGQVLERGPVLQLHDLKREAGGGYRCVAS
                                                                                     REAEEETTNDNGVLVLEPARKEHSGRYECQGLDLDTMISLLSEPQELLVNYVSDVRVSPA
                                                                                                                                                                             GRVLQPVEEVVVINLRKVEN-RSTGLFTMTSSLQYMPTKEDANAKFTCIVTYHGPSGQKT
                                                                                                                                                                                                                                      DDVSEEPTV-VKVFKQPSQPEILHQADFL----ETEKLKMLGECVVRDSYPEGNVTWYKN
                                                                                                                                                                                                                                                                                                                                                       LLC--LLLAALCMPPALGL-----YTVNAVYGDTITMPCRLEVPDG-LMFGKWKYE 65
                                                                                                                                                                                                                                                                                                                                                                                                                166;
                                                                                                                     IQSEPVVFDVHYPTEKVTIRVLSQSSTIKEGDNVTLKCSGNGNPPPQEFLFYI-----
                                                         -PGETEGIRSSDTYVMTDVRRNATGEYKCSLIDKSMM-----DTTTITVHYL-DLQLTPS
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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26.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                  116;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 505.5; DB 2;
Pred. No. 7.7e-25;
6; Mismatches 255;
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C;Accession: JH0464
R;Burns, F.R; von Kannen, S.; Guy, L.; Raper, J.A.; Kamholz, Reuron 7, 209-220, 1991
A;Title: DM-GRASP, a novel immunoglobulin superfamily axonal A;Reference number: JH0464; MUID:91337449
A;Accession: JH0464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
JH0464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Comment: This is a cell surface glycoprotein. C;Comment: This protein is localizes to axons in C;Comment: glycoprotein C;Keywords: glycoprotein C;Keywords: glycoprotein e;1-32/Domain: signal sequence #status predicted F;33-887/Product: DM-GRASP #status predicted <DMCF;67,198,270,311,365,461,484,503/Binding site: ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Gallus gallus (chicken)
C; Date: 31-Mar-1992 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-587 <BUR>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPSIPGLNRTQLVNVAIFGPPWMAFKERKVWVKENMVLNLSCEASGHPRPTISWNVNGTA 470
                                                                                                                                                                                                                                                                                                                              GRPLK--EEKNRVHIQSSQTVESSGLYTLQSILKAQLVKEDKDAQFYCELNYRLPSGNHM
                                                                                                                                                                                                                                                                                                                                                                                                                          RPRSQEYRIQLRVYKAPEEPNI--QVNPLGIPVNSKEPEEVATCVGRNGYPIPQVIWYKN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTVTSLNVSAISIPEYDEPEDR-NDDNSEK----VNDQAKLIVGIVVGLLLVALVAGVVY
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                                                                                                                                                                                                                                           KESREVTVPVFYPTEKVWLEV-EPVGMLKEGDRVEIRCLADGNPPPH---FSISKQNPST
                                                                                                                                                                                                                                                                                                                                                                                         DDVSEEPTV-VKVFKQPSQPEILHQADFL----ETEKLKMLGECVVRDSYPEGNVTWYKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLY-KKGKLPCRRSGKQEITLPPSRKSE 607
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VPSIPGLNRTQLVNVAIFGPPWMAFKERKVWVKENMVLNLSCEASGHPRPTISWNVNGTA 470
                                            GEVTKQIGEALPVSCTISSSRNATVFWIKDNTR--MKTSP--SFSSLQYQDAGNYICETT
                                                                                   AP-ERQEGSSLTLTCEAESSQDLEFQWLREETGQVLERGPVLQLHDLKREAGGGYRCVAS 410
                                                                                                                             -PGETEGIRSSDTYVMTDVRRNATGEYKCSLIDKSMM-----DATTITVHYL-DLQLTPS
                                                                                                                                                                   REAEEETTNDNGVLVLEPARKEHSGRYECQGLDLDTMISLLSEPQELLVNYVSDVRVSPA 351
                                                                                                                                                                                                                     IQSEPVVFDVHYPTEKVTIRVLSQSSTIKEGDNVTLKCSGNGNPPPQEFLFYI-----
                                                                                                                                                                                                                                                                                                      GRVLQPVEEVVVINLRKVEN-RSTGLFTMTSSLQYMPTKEDANAKFTCIVTYHGPSGQKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VHKEKRTLI-FR--VRQGQGQSEPGEYEQRLSLQDRGATLALTQVTPQDERIFLCQ--GK 119
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    chicken

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 502.5; DB 2
Pred. No. 1.2e-24;
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carbohydrate
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A; Residues: 1-583 <RES>
A; Cross-references: GB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSTALLKCGLSQSQGNLSHVDWFSVHKEKRTLIFRVRQGQGQS----EPGEYEQRLSLQD
                         QLERTVNSLNVSAISI ---
                                                DLGKNTSILFLELVNLTTLTPDSNTTTGLSTSTASPHTRANSTSTERKLPEPESRGVVIV 563
                                                                              IICHVEGFPKPAIQWTITGSGSVINQTEESPYINGRYYS--KIIISPEENVT-LTCTAEN
                                                                                                 LSCEASGHPRPTISWNVNGTAS---EQDQDPQ---RVLSTLNVLVTPELLETGVECTASN
                                                                                                                                   P--SFSSLHYQDAGNYVCETALQEVEGLKKRESLTLIVEGKP--QIKMTKKTDPSGLSKT
                                                                                                                                                              PVLQLHDLKREAGGGYRCVASVPSIPGLNRTQLVNVAIFGPPWMAFKERKVWVKENMVLN
                                                                                                                                                                                        STA----ITVHYL-DLSLNPSGEVTRQIGDALFVSCTISASRNATVVWMKDNIR---LRSS
                                                                                                                                                                                                                    LLSEPQELLVNYVSDVRVSPAAP-ERQEGSSLTLTCEAESSQDLEFQWLREETGQVLERG
                                                                                                                                                                                                                                                  GNGNPPPEEFLFYLPGQPEGIRSSNTYTLMD------VRRNATGDYKCSLIDKKSMIA
                                                                                                                                                                                                                                                                           ADGNPPPH---FSISKQNPSTREAEEETTNDNGVLVLEPARKEHSGRYECQGLDLDTMIS
                                                                                                                                                                                                                                                                                                        ADIQMPFTCSVTYYGPSGQKTIHSEQAVFDIYYPTEQVTIQVLPPKNAIKEGDNITLKCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDTIIIPCRLDVPQ-NLMFGKWKYEKPDGSPVFIAFRSSTKKSVQYDDVPEYKDRLNLSE
                                                                                                                                                                                                                                                                                                                                    EDKDAQFYCELNYRLPSGNHMKESREVTVPVFYPTEKVWLEV-EPVGMLKEGDRVEIRCL
                                                                                                                                                                                                                                                                                                                                                                 KKLGDCISEDSYPDGNITWYRNGKVLHPLEGAVVIIFKKEMDPVTQLYTMTSTLEYKTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                RGATLALTQVTPQDERIFLCQ-GKRPRSQEYRIQLRVYKAPEEPNIQVNPLGIPVNSKEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S--EQDQDPQRVLSTLN--VLVTPELLETGVECTASNDLGKNTSILFLELVNLTTLTPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                      -NYTLSISNARISDEKRFYCMLYTEDNYFEAPTIVKYFKQPSKPEIVSKALFL--ETEQL
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Pred. No. 5.2
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                       -HDEADEISDENR-EKVNDQAKLIV
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hypothetical protein F15G9.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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RESULT
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Differentiation 56, 21-29, 1994
A; Title: Molecular characterization of fish
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A;Molecule type: mRNA
A;Residues: 1-523 <LAE>
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Best Local S
Matches 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 GSTALLKC--GLSQSQGNLSHVDWFSVHKEKRTLIFRVRQGQGQ----SEPGEYEQRLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GETIVVPCNDGTKKPDG-LIFTKWKYVKDDGSPGDLLVKQAQKDEATVSATDGYKSRVSI
                                                         QAKVIVGIVVGLLVAAALVGLIYWIYIKKTRQGSWKTGEKEAGTSEESKKLE
                                                                            RKVWWKENMVLNLSCEASGHPRPTISWNVNGTASEQDQDPQRVLSTLNVLVTPELLETGV
                                                                                                                                                                                                                                         D--NRKLDKLP--DFSKLTYSDAGLYVCDV---SIEGIKRSLSFELTVEGIPKITSLTKH
                                                                                                                                                                                                                                                                                                                                QGLDLDTMISLLSEPQELLVNYVSDVRVSPAAPE-RQEGSSLTLTCEAESSQDLEFQWLR
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                                                                                                                     SCLVTNKLGEDTKEI
                                                                                                                                                                             RSSDGKHKV---LTCEAEGSPKPDVQWSVNGTNDEVSYNNGKATYKLTVVPSKNLT---V
                                                                                                                                                                                                                                                                       EETGQVLERGPVLQLHDLKREAGGGYRCVASVPSIPGLNRTQLVNVAIFGPPWMA--FKE
                                                                                                                                                                                                                                                                                                     SLLDNDVMES - - - - TQFVTVSFL - DVSLTPTGKVLKNVGENLIVSLDKNASSEAKVTWTK
                                                                                                                                                                                                                                                                                                                                                                                     EGDRVEIRCLADGNPPP---HFSISKQNPSTREAEEETTNDNGVLVLEPARKEHSGRYEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELENGKLTQLGECVVENANPPADLIWKKNNQTLVDDGKTIIITSTITKDKITGLSSTSSR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDRGATLALTQVTPQDERIFLCQ-GKRPRSQEYRIQLRVYKAPEEPNIQVNPLGIPVNSK 153
                                                                                                                                                ECTASNDLGKNTSILFLELVNLTTLTPDSNTTTGLSTSTASPHTRANSTSTERKLPEPES
                                                                                                                                                                                                                                                                                                                                                                  EGEDVTLKCQADGNPPPTSFNFNI------KGKKVTVTDKDVYTLTGVTRADSGIYKC
                                                                                                                                                                                                                                                                                                                                                                                                                            LQYTARKEDVESQFTC-----TAKHVMGPDQVSEPESFPIHYPTEKVSLQVVSQSPIR
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26.7%;
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Pred. No. 8.3e-22,
08; Mismatches 220
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A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-5175 <WIZ>
A:Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.
A:Experimental source: Clone T09B9
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R;Sulston, J.
submitted to the EMBL Data Library,
A;Reference number: Z19355
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A;Residues: 1-5175 <WIL>
A;Cross-references: EMBL:247068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a
A;Experimental source: clone F15G9
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RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                   CVASVPSIPGLNRTQLVNV---AIFGPPWMAFKERKVWVKENMVLNLSCEASGHPRPTIS 463
                                                                                                                                                                                                                                                                                                                                              GLTLHFDSVSVKQEGNYHCVAQSKGNILDIDVELSVLAVP···IVGEDDNLEVF----
                                                                                                                                                                                                                                                                                                                                                                                                                      NLDESKYKKKV----FAKEGEEVTLGCPVSGFPVPQINWVVDGTVVEPGKKYKGATLSND
                                                                                                                                                                                                                                                                                                                                                                                                                                         FYPTEKVWLEVEPVGMLKEGDRVEIRCLADGNPPPHFSI----SKQNPSTREAEEETTND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLHVFKAK-ITDSGVYKCVA--
                                                                                     TTLTPDSNTTT
                                                                                                                           WKIDGNDVDKSWLFDESLSLLRI --
                                                                                                                                                           WNVNGTASEQDQDPQRVLSTLNVLVTPELLETG - - - - VECTASNDLGKNTSILFLELVNL
                                                                                                                                                                                                                                                                         - LGKDISLSCDLQTESDDKTTFVWSINGSESDRPDNVQIPSDGHRLYITDAKPENNGKYM
                                                                                                                                                                                                                                                                                                          QEGSSLTLTC--EAESSQDLEFQWL------REETGQVLERGPVLQLHDLKREAGGGYR 406
                                                                                                                                                                                                                                                                                                                                                                              NGVLVLEPARKEHSGRYECQG------LDLDTMISLLSEPQELLVNYVSDVRVSPAAPER
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                                                   PTEKNEGDQET
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                                                   1836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 281; DB 2; Length 5175; Pred. No. 3.6e-09; 91; Mismatches 220; Indels 11
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R; Kershaw, J.
R; Kershaw, J.
submitted to the EMBL Data
submitted to number: Z19929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: 222396
A; Accession: T43290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, June 1998 A;Description: Hemicentin is required for hemidesmosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hemicentin precursor - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 C;Accession: T43290; T20993; T24734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-5198 <WI2>
A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; A;Experimental source: clone T09B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-5198 <WIL>
A; Cross-references: EMBL: Z47068; PIDN: CAA87336.1; GSPDB: GN00028; CESP: F15G9.4b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: T20993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-5198 < VOG>
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Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: clone F15G9
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Best Local S
Matches 122
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  CVASVPSIPGLNRTQLVNV---AIFGPPWMAFKERKVWVKENMVLNLSCEASGHPRPTIS
                                                                                                                                      GLTLHFDSVSVKQEGNYHCVAQSKGNILDIDVELSVLAVP---IVGEDDNLEVF-----
                                                                                                                                                                                                                                                          KLHVFKAK-ITDSGVYKCVA--
                                                                                                                                                                                                                                                                                                                                                                                                                       IKDPDVVTQE---SIKESHPFSLYCPVFSN--PLPQISWYLNDKPLIDDKTSWKTSDDKR 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                --EPNIQVNPLGIPVNSKEPEEVATCVGRNGYPIPQVIWYKNGRPL-----KEEKN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary;
                                             -LGKDISLSCDLQTESDDKTTFVWSINGSESDRPDNVQIPSDGHRLYITDAKPENNGKYM
                                                                                      QEGSSLTLTC--EAESSQDLEFQWL-----REETGQVLERGPVLQLHDLKREAGGGYR 406
                                                                                                                                                                                    NGVLVLEPARKEHSGRYECQG------LDLDTMISLLSEPQELLVNYVSDVRVSPAAPER
                                                                                                                                                                                                                                NLDESKYKKKV----FAKEGEEVTLGCPVSGFPVPQINWVVDGTVVEPGKKYKGATLSND
                                                                                                                                                                                                                                                                                                                                                                    RVHIQSSQTVESSGLYTLQSILKAQLVKEDKDAQFYCELNYRLPSGNHMKESR-EVTVPV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIGTDTKG-----YVVESDGTLVIQSASVEDATIYTCKASNPAGKAEANLQVTVIASPD 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVQEPPIILPSTQTNNTAVVGDRVELKCYVEASPP---ASVTWF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
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Pred. No. 3.6e-09;
1; Mismatches 220
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A49448
AFference number: A49448; S34129
R. Ramos, R.G.P.; Igloi, G.L.; Lichte, B.; Baumann, U.; Maier, D.; Schneider, T.; Brandst Genes Dev. 7, 2533-2547, 1993
A;Title: The irregular chiasm C-roughest locus of Drosophila, which affects axonal projections A49448; A;Accession: A49448; MUID:94102535
A;Accession: A49448; MUID:94102535
A;Accession: A49448
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A;Cross-references: FlyBase:FBgn0003285
C;Keywords: transmembrane protein
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A; Residues: 1-764 < RAM>
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SGHDYSILVDAVPGGVKSTLIIRDSQAYHYGKYNCTVVNDYGNDVAEIQLQAKKSVSL--
                                 QDQD-------PQRVLSTLNVLVTPELLETGVECTASNDLGKNTSILFLELVNLTTLTP 524
                                                                                                                                                                                                                    QEGSSLTLTCEAESSQDLEFQWLREETGQVLERGPVLQLHDLKREAGGGYRCVASVPSIP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVE---IECVSVGGKPAAEITWIDGLGNVLTDNIEYTVIPLPDQRR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SLDIYPVMLDDDARYQCQVSPGPEGQPAIRSTFAGLTVLVPPEAPKITQGDVIYATADR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATLALTQVTPQDERIFLCQGK-----RPRSQEYRIQLRVYKAPEEPNIQVNPLGIPVNSK
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                                                                                         EISADAYVYLK--GSPAIG-SQRTQYGLVGDTARIECFASSVPRARHVSWTFNGQEISSE 473
                                                                                                                                     GINRTQLVNVAIFGPPWMAFKERKVWVKENMVLNLSCEASGHPRPT-ISWNVNG--TASE 472
                                                                                                                                                                                  DVGSVVSLTCEVDSNPQPEIVWIQHPSDRVVGTSTNLTF-SVSNETAGRYYCKANVPGYA 416
                                                                                                                                                                                                                                                                            TE-----MVIRNVTRKFHDAIVKC---EVQNSVGKSEDSETLDISYAPSFRQRPQSMEA
                                                                                                                                                                                                                                                                                                                        EETTNDNGVLVLEPARKEHSGRYECQGLDLDTMISLLSEPQELLVNYVSDVRVSPAAPER 355
                                                                                                                                                                                                                                                                                                                                                                     LPGGAGGSVGGAGGGSVHMSTGSRIVEHSQVRLECRADANPSDVRYRWFINDEPIIGGQK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTAKSVLRLTPKKEHHNTNFSCQAQ---NTADRTYRSAKIRVEVKYAPK---VKVNVMGS 246
                                                                                                                                                                                                                                                                                                                                                                                                                   ----DRVEIRCLADGNPPP--HFSISKQNPSTREAE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 158;
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	YTIHRARLADAGVYECESKNEIGLQLRSITLDVKGRESN 490	451 A	рь
	LVTPELLETGV-ECTASNDLGKNTSILFLELVNLTTLTPDSNTTTGLSTSTASPHTR 542	487 I	Qy
	WMAFKERKVWVKENMVLNLSCEASGHPRPTISWNVNGTASEQDQDPORVLSTLNV 486	431 P 399 P	Qy Db
	EFQWLREETGQVLERGPVLQLHDLKREAGGGYRCVASVPSIPGLNRTQLVNVAIFGP 430 :	374 E 342 K	Qy
	RYECQGLDLDTMISLLSEPQELLVNYVSDVRVSPAAPERQEGSSLTLTCEAESSQDL 373 	317 R 286 I	Qy
	EPVGMLKEGDRVEIRCLADGNPPPHFSISKQNPSTREAEEETTNDNGVLVLEPARKEHSG 316 	257 E 229 N	Db -
	ESSGLYTLQSILKAQLVKEDKDAQFYCELNYRLPSGNHMKESREVTVPVFYPTEKVWLEV 256 	197 E	Qy Db
	NPLGIPVNSKEPEEVATCVGRNGYPIPQVIWYKNGRPLKEEKNRVHIQSSQTV 196 : : : : : : : : :	144 N 125 S	Qy Db
	RLSLODRGATLALTOVTPQDERIFLCQGKRPRSQEYRIQLRVYKAPEEPNIQV 143 ::	91 F 71 K	Db Oy
	PAPELVEVEVGSTALLKCGLSQSQGNLSHVDWFSVHKEKRTLIFRVRQGQGGSEPGEYEQ 90 ::: :: :	31 P 31 P	Qy Db
27;	7.9%; Score 264.5; DB 2; Length 538; Similarity 21.6%; Pred. No. 1.8e-09; 6; Conservative 103; Mismatches 234; Indels 119; Gaps 2	547	Que Bes Mat
molecule	JC2457 I.M.; Haskard, D.O.; Robinson, M.K. phys. Res. Commun. 201, 805-812, 1994 ping and expression kinetics of porcine vascular cell adhesion number: JC2457; MUID:94271236 JC24870 JC24870 JC24871 1-538 <tsa> 2 rences: EMBL:U08351; NID:9474382; PIDN:AAA21542.1; PID:9474383 glycoprotein; transmembrane protein maain: transmembrane #status predicted <tmm></tmm></tsa>	Accession Tsang, Y.7 Cohem. Bid Title: Cld Reference Accession Molecule t Residues: Cross-ref Keywords: 497-517/Dd 75,157,277	C; Acc R; Tsa Bioch A; Rit A; Acc A; Acc A; Res A; Res C; Key C; Key F; 4,97 F; 7,57
	pig (domestic pig)	457 cular ce pecies:	RES JC2 Vas
	598	598 K	Db -
	645	645 R	Qy
	KGKLPCRRSGKQEITLPPSRKSELVVEVKSDKLPEEMGLLQGSSGDKRAPGDQGEKYIDL 644	585 F	Db -
	LMTIVGG555	532 -	Db
	VCILVLAVLGA	525 I	Qy

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A; Title: Characterization of a member of the A; Reference number: A39712; MUID:91271300 A; Accession: A39712
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A39712
kinase-like
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A; Residues: 1-1051 <CHO>
A; Cross-references: GB: M63437; NID: g212235; PIDN: AAA48933 1; PID: g212236
A; Cross-references: GB: M63437; NID: g212235; PIDN: AAA48933 1; PID: g212236
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein
C; Keywords: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase-like protein klg precursor - chicken C; Species: Gallus gallus (chicken) C; Date: 08-Nov-1991 #sequence_revision 08-Nov-1991
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R; Chou, Y.H.; Hayman, M.J
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F;783-791/Region: protein kinase ATP-bindir
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nes 149; Conserv
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AGNSCNIKHREAFLYVVDKPAAEEDEG
                                                                                                CEASGHPRPTISWNVNGTASEODODPORVLSTLNVLVTPELLETGVECTASNDLGKNTSI
                                                                                                                                   FHKVSRSDSGNYTCIASNSPQGEIRATVQLVVAVY----VTFKLEPEPTTVYQGHTAMFQ
                                                                                                                                                                   LHDLKREAGGGYRCVASVPSIPGLNRTQLVNVAIFGPPWMAFK--ERKVWVKENMVLNLS
                                                                                                                                                                                                                                                                    RNGVSISEDSRFEISENGTLRINNVEVYDGTMYKC-----VSSTPAGSIEGYARV
                                                                                                                                                                                                                                                                                                     KONPSTREAEEETTNDNGVLVLEPARKEHSGRYECOGLDLDTMISLLSEPQELLVNY---
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                                                                                                                                                                                                                                                                                                                                                                                                       WWERNOERVPTAGRVYQEAEQLVF--TSITEADAGIYTCHAANKA-----
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                                                               CQAEGDPVPHIQWK----GKDKILDPSKLLPRIQIMPNGSLV---IYDVTTEDSGKYTCI
                                                                                                                                                                                                   HVLEKLKFTPPPQPLQCMEFNKEVTVSCSATGREKPTIQWTKTDGSSLPSHVSHRAGILS
                                                                                                                                                                                                                                    -- VSDVRVSPAAPERQ---EGSSLTLTCEAESSQDLEFQWLREE----TGQVLERGPVLQ
                                                                                                                                                                                                                                                                                                                                      ---GEKKQELSITV----ATVPKWVEMPKDSQLEESKPGYLHCLSKASLKPTVTWY
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                             -LFLELVNLTTLTPDSNTTTGLSTSTASPHTRANSTSTERKLPEPESRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                         -GRPLKEEKNRVHIQSSQTVESSGLYTLQSILKAQLVKEDKDAQFYCEL
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Pred. No. 9.4e-09;
9; Mismatches 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neural cell adhesi N; Alternate names:
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8
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F;149-153/Region: heparin binding #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-1088 <KRI>
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NGRPLKEEKNRVHIQSSQTVESSGLYTLQSILKAQLVKEDKDAQFYCELNYRLPSGNHMK 236
                                   EGRILARGEINYKDIQVIVNVPPTIQARQLRVNATANMAESVVLSCDADGFPDPEISWLK
                                                                                                  KEGEDAVIICDVSSSIPSIITWRHKGKDVIFKKDVRFVVLANNYLQIRGIKKTDEGTYRC 186
                                                                                                                                                                     SVVRSDDYTSTLTIYNASSQDAGIYKCVASNEAEGESEGTVNLKIYQKLTFKNAPTPQEF 126
                                                                                                                                                                                                      SL---QDRGATLALTQVTPQDERIFLC-----QGK-----
                                                                                                                                                                                                                                      PDQGEISLGESKFFLC---QVSGEATDISWYSPTGEKLVT--
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                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                        7.6%;
18.1%;
                                                                                                                                                                                                                                                                                                         100;
                                                                 PNIQVNPLGIPVNSKEPEEVATCVGRNGYPIPQVIWYK 176
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Pred. No. 1.7e
)0; Mismatches
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No. 1.
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-IQLRVYKAPEE---- 138

246

-----RPRSQEY 126

-----QQQI 66

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A:Cross-references: EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g214610
A:Note: the authors translated the codon AAA for residue 970 as Leu
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with anc
C:Comment: Several forms of NCAM are produced by alternative splicing.
C:Genetics:
A:Gene: NCAM
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat h
C:Keywords: alternative splicing; brain; cell adhesion; duplication; hepari
F:1-19/Domain: signal sequence #status predicted <SIG>F:20-803,1050-1088/Product: neural cell adhesion molecule, short domain for
F:20-108/Product: neural cell adhesion molecule, short domain for
F:30-705/Domain: extracellular #status predicted <EXT>
F:30-705/Domain: immunoglobulin homology <IMMI>
F:30-108/Product: immunoglobulin homology <IMMI>
F:30-108/Product: immunoglobulin homology <IMMI>
F:30-108/Promain: immunoglobulin homology <IMMI>
F:30-108/Promain: immunoglobulin homology <IMMI>
F:30-108/Promain: immunoglobulin homology <IMMI>
F:30-108/Promain: immunoglobulin homology <IMMI>
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                                                                                                                                                                                                                                                                        F;512-589/Domain: fibronectin type III repeat homology <FN3A>F;618-679/Domain: fibronectin type III repeat homology <FN3B>F;706-723/Domain: transmembrane *status predicted <TMM>F;706-723/Domain: intracellular *status predicted <TMM>F;724-1088/Domain: intracellular *status predicted <TMM>F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: *status predicted <TMM>F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: *status predicted <TMMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;149-153/Region: heparin binding #status predicted F;158-162/Region: heparin binding #status predicted F;258-284/Domain: immunoglobulin homology <IMM3> F;317-381/Domain: immunoglobulin homology <IMM4> F;413-475/Domain: immunoglobulin homology <IMM5>
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PELVEVEVGSTALLKCGLSQSQGNLSHVDWFSVHKEKRTLIFRVRQGQGQSEPGEYEQRL 92
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.7e-08;
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uplication; heparin binding;
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Db	Qy	DЬ	Qγ	Db	Qy	Db	Ωу	В	Qy	DЬ	Qy	рЬ	Qy	Дb	Qу	Вb	Qy	Db	Qy	В
779	627	732	584	695	524	635	484	575	456	515	430	455	392	398	. 342	346	297	290	237	247
EERTPNHDGSNQIE 792	SSGDKRAPGDQGEKYID 643	KCGLLMCIAVNFCGKAGPGAKGKDIEEGKAAFSKDESKEPIVEVRTE 778	KKGKLPCRRSGKQEITLPPSRKSELVVEVKSDKLPEEMGLLQG 626	ATASAGTGLGTG731	PDSNTTTGLSTSTASPHTRANSTSTERKLPEPESRGVVIVAVIVCILVLAVLGAVLYFLY 583	LNALEWKPEMRVPSNSHHVMLKALEWNVDYEVIVVAENQQGKSKPALLSFRTTAKPTATT 694	LNVLV-TPELLETGVECTASNDLGKNTSILFLELVNLTTLT 523	GKGLGDSTPSQEFTTQPVREPSAPKLVGHLSEDGNSIKVDILKQDDGGSPIRHYLVNVRA 634	GHPRPTISWNVNGTASEODQDPQRVLST 483	EPDSTGGVPILKYKAEWRVIGHEKWHTKYYDAKEVNAESIITVMGLKPETSYMVKLSAMN 574	PPWMAFKERKVWVKENMVLNLSCEAS 455	SSSLEVNPDSENDFGNYNCTAINTIGHEFSEFILVQADTPSSPAIRKVEPYSSTVMTVFD 514	LQLHDLKREAGGGYRCVASVPSIPGLNRTQLVNVAIFG 429	YAPKIR-GPVVVYTWEGNPVNITCEVFAHPRAAVTWFRDGQLLPSSNFSNIKIYSGPT 454	YVSDVRVSPAAPERQEGSSLTLTCEAESSQDLEFQWLREETGQVLERGPV 391	ATTLDGHIVVKEHIRMSALTLKDIQYTDAGEYFCIASNPIGVDMQAMYFEVQ 397	ETTNDNGVLVLEPARKEHSGRYECQGLDLDTMISLLSEPQELLVN 341	EAEATILLKVYAKPKITYVENKTAVELDEITLTCEASGDPIPSITWRTAVRNISSE 345	ESREVTVPVFYPTEKVWLEVEPVGMLKEGDRVEIRCLADGNPPPHFSISKQNPSTREAEE 296	::: : ::

Search completed: March 23, 2001, 12:31:19 Job time: 42 sec

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Listing first 45 summaries
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					1 MAN	SULT 1 18_HUMAN
	ABAGNITENIS			*		
	AT TONING OFFICE					
	NEO1_MOUSE	1	1493	6.0	202.5	45
	DCC_MOUSE	Н	1447	6.0	203	44
	NGCA_CHICK	ш	1266	6.1	203.5	43
	DSCA_HUMAN	ட	2012	6.1	204.5	42
Q28173 bos taurus	RAGE_BOVIN	ᅩ	416	6.1	204.5	41
P35968 homo sapien	VGR2_HUMAN	بــر	1356	6.1	205.5	40
063495 rattus norv	RAGE_RAT	μ.	402	6.1	205.5	39
	BGP1_HUMAN	_	526	6.2	207	38
mus	VCA1_MOUSE	_	739	6.2	208	37
	CD22_MOUSE	μ.	862	6.2	209	36
	VGR1_MOUSE	Ļ	1333	6.2	210	35
P20273 homo sapien	CD22_HUMAN	1	847	6.4	214	34

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-!- TISSUE SPECIFICITY: MAY APPEAR AT THE SURFACE OF NEURAL CREST CELLS DURING THEIR EMBRYONIC MIGRATION. APPEARS TO BE LIMITED TO CELLS DURING THEIR EMBRYONIC MIGRATION. APPEARS TO BE LIMITED TO VASCULAR SMOOTH MUSCLE IN NORMAL ADULT TISSUES. ASSOCIATED WITH TUMOR PROGRESSION AND THE DEVELOPMENT OF METASTASIS IN HUMAN MALIGNARY MELANOMA. EXPRESSED MOST STRONGLY ON METASTATIC LESIONS AND ADVANCED PRIMARY TUMORS AND IS ONLY RAFELY DETECTED IN BENIGN MELANOCYTIC NEVI AND THIN PRIMARY MELANOMAS WITH A LOW PROBABILITY OF METASTASIS.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 3 C2-LIKE AND 2 V-LIKE DOMAINS.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD146 entry; WMW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd146.htm".
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MEDLINE=95042297; PubMed=7954395;
Campbell I.G., Foulkes W.D., Senger
Garin-Chesa P., Rettig W.J.;
"Molecular cloning of the B-CAM cel
epithelial cancers: a novel member
                                                                                                                                                                                                                               P50895;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-HERAN BLOOD GROUP GLYCOPROTEIN PRECURSOR (B-CAM CELL
GLYCOPROTEIN) (AUBERGER B ANTIGEN) (F8/G253 ANTIGEN).
LU OR BCAM OR MSK19.
                                                                                                            Parsons S.F., Mallinson G., Holmes C.H., Houlihan Mawby W.J., Spurr N.K., Warne D., Barclay A.N., A "The Lutheran blood group glycoprotein, another m immunoglobulin superfamily, is widely expressed is developmentally regulated in human liver."; proc. Natl. Acad. Sci. U.S.A. 92:5496-5500(1995).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- FUNCTION: PROBABLE RECEPTOR. MAY MEDIATE INTRAELLULAR
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION (HIGHEST

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LAYER OF
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SIMILARITY:
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                                                    NGYPIPQVIWYKNGRPLK--EEKNRVHIQSSQTV-ESSGLYTLQSILKAQLVKEDKDAQF
                                                                                 QVGDERDYVCVVRAGAAGTAEATARLNVFAKPEATEVSPNKGTLSVMEDSAQEIATCNSR
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CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE DOMAIN.

IG-LIKE V-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                 PROBABLE.
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
RL -> PC
RL -> DV
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PROBABLE.
PROBABLE.
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                                                                                                                                                                                                                                                                                        C89B0A4835492B1E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                 GLCNAC . . . )
                                                                                                                                                                                                                                          .5e-35;
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                                                                                                                                                                                                                                                                                       CRC64;
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RESULT 3
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01-NOV-1995
15-JUL-1999
                                           POSSIBLE FUNCTION.
MEDLINE=92211411; PubMed=1313497;
                             Pourquie O.,
                                                                                                                  Pourquie O., Corbel C., le Caer J.-P., Rossier J., "BEN, a surface glycoprotein of the immunoglobulin expressed in a variety of developing systems.", proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).
                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                       "DM-GRASP, a novel immunoglobulin that supports neurite extension."; Neuron 7:209-220(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuron
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tanaka H., Matsui T., Agata A., Tomura M., Kubota I., McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton McJarland cloning and expression of a novel adhesion mc Neuron 7:535-545(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD166 ANTIGEN EGRASP PROTEIN)
                                                                                                                                                                                                               MEDLINE=92302224;
                                                                                                                                                                                                                                     TISSUE=BURSA OF FABRICIUS;
                                                                                                                                                                                                                                                                                                                                                                                                    Burns F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91337449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken)
    'Association
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92030150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGVAVMAVAVSVGLLLLVVAVFYCVRRKGG-PCCRQRREKGAPPP---GEPGLSHSGSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGVVIVAVIVCILVLAVLGAVLYFLYKKGKLPCRRSGKQEITLPPSRKSELVVEVKSDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCEASNPHGNKRHVFHFGAVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W-REGDEVTLICSARGHPDPKLSWSQLG-GSPAEPIPGRQGWVSSSLTLKVTSALSRDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WVKENMYLNLSCEASGHPRPTISWNVNGTASEQDQDPQR----VLSTLNVLVTPELLETGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGDGPMLSLSSITFDSNGTYVCEASLPTVPVLSRTQNFTLLVQGSPELKTAEIEPKADGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTLELRVAYLDPLELS-----EGKVLSLPLNSSAVVNCSVHGLPTPALRWTKDST--P 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPSPEYTLFR----LQDEQEEVLNVNLEGNLTLEGVTRGQSGTYGCRVEDYDAADDVQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPPPHFSISKQNPSTREAEEETTNDN--GVLVLEPARKEHSGRYECQGLDLDTMISL-LS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LERGPVLQLHDLKREAGGGYRCVASVPSIPGLNRTQLVNVAIFGPPWMAFKERK-----V 440
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                      von
Hallonet M.E.R., le of BEN glycoprotein
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Rel. 32, Last sequence update)

Rel. 38, Last annotation update)

Rel. 38, CSCI GLYCOPROTEIN) (BEN GLYCOPROTEIN) (DM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JC7 PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                                    Kannen
                                                                                                                                                                                                             PubMed=1608932;
                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1873027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=1931049;
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                                                                                                                                                                                                                                                        OF 34-52;
                     Douarin
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                                                                                                                                                                                                                                                                                                                                                     superfamily
                                                                                                                                                                                                                                                                                                                                                                                                 Raper J.A.,
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Best L
                                                Matches
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J. Neurosci. 12:1548-1557(1992).

-!- FUNCTION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING FIBER AXONOGENESIS. SUPPORTS NEURITE EXTENSION.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.

-!- TISSUE SPECIFICITY: EXPRESSED IN A RESTRO AXONS IN THE DORSAL FUNICULUS, MUDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND IN EPUTHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH EPUTHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH EPUTHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH EPUTHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH
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CARBOHYD
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CARBOHYD
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DISULFID
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DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN
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DOMAIN
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INTERPRO; IPRO03006; -.
PFAM; PF00047; ig; 5.
PROSITE; PS00290; IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS002
Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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Local
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OF BEN.
DEVELOPMENTAL
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M76678; AAA48602.1;
X64301; CAA45579.1;
Q13740; IKJC
                        LVCAFLLAACCCCPRVAGVPGEAEQPAPELVEVEVGSTALLKCGLSQSQGNLSHVDW-FS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. C2-LIKE AND 2 V-LIKE DOMAINS.
                                                             Similarity
                                                                                                                         163
2776
359
3440
101
1173
1173
312
3166
2271
3166
2271
250
4485
271
1123
271
271
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JO; IG_MHC; FALSE_NEG.
Immunoglobulin domain;
                                                                                                       199
312
316
366
462
485
485
504
10
25
113
329
402
65726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STAGE: WIDELY EXPRESSED
                                                            15.2%;
                                                                                                             MΨ:
                                                                                                            MEPPAAAAR -> EPPSRRRP (IN I
A -> S (IN REF. 3).
SD -> RH (IN REF. 3).
A -> T (IN REF. 2).
LQ -> HK (IN REF. 2).
W; 2A28612D0164531E CRC64;
                                                                                                                                                                                                                                                                                                        IG-LIKE V-TYPE DOMAIN.
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                Score 509.5;
Pred. No. 1.8e
L7; Mismatches
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N-LINKED
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O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
                                                               SEQUENCE Or .... PubMeu---- Sijzen MEDLINE-98161527; PubMeu---- Sijzen Degen W.G., van Kempen L.C., Gijzen Van Kooyk Y., Bloemers H.P., Swart G van Kooyk Y., B
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Haynes B.F
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          molecule)
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Wang W.-C., Marquardt H.,
Haynes B.F., Aruffo A.;
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Mammalia; Eutheria; Primates;
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          Pathol.
          152:805-813(1998)
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empen L.C., Gijzen E.G.
emers H.P., Swart G.W.;
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"MoLecular model of the N-terminal receptor-binding domain human CD6 ligand ALCAN.";
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MEDLINE=96420463; PubMed=8823162;
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CD6-BINDING
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DATABBASE: NAME=PROW; NOTE=CD guide CD166
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CAA71256.1;
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                                                  MEDITNE-97353242; PubMed-9209500; Bowen M.A., Bajorath J., D'Egidio M., Whitney G.S., Palmer Bowen M.A., Bajorath J., Siaddak A.W., Aruffo A.; "Characterization of mouse ALCAM (CD166): the CD6 binding conserved in different homologs and mediates cross-species Eur. J. Immunol. 27:1469-1478(1997).
                                                                                                                                                                                                                                                       C166_MOUSE STANDARD; PRT; 583 AA. Q61490; O70136; Q1-NOV-1997 (Rel. 35, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL
SEQUENCE OF 227-583 FROM N.A. STRAIN-BALB/C; TISSUE-BRAIN; MEDLINE-94376084; PubMed-8089
                                             Eur. J.
[2]
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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24.8%;
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                                                                                                                                                                                   Craniata; Vertebrata; | Sciurognathi; Muridae;
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Pred. No. 2.
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Matches 152
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"The molecular cloning and characterization of ppm-GRASP homologs in zebrafish and mouse.";
J. Neurobiol. 25:831-845(1994).
-1- FUNCTION: CELL ADHESION MOLECULE THAT BINDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entitles requires a license agreement
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
3 C2-LIKE AND 2 V-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEURITE EXTENSION BY NEURONS VIA INTERACTIONS. MAY PLAY A ROLE IN ACTIVATED LEUKOCYTES, AS WELL AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATED LEUKOCYTES, AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:1313266; ALCAM. RPRO; IPRO00495; -.
                                                                                                                                                                                                                                               RLVCAFLLAACCCCPRVAGVPGEAEQPAPELVEVEVGSTALLKCGLSQSQGNLSHVDWFS
                                                                                                                                                             VHKEKRTLIFRVRQGQGQS----EPGEYEQRLSLQDRGATLALTQVTPQDERIFLCQ-GK
                                                                                                                                                                                                                                                                                       152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U95030; AAC06342.1; -. L25274; AAA37528.1; -.
                                                                             RPRSQEYRIQLRVYKAPEEPNIQVNPLGIPVNSKEPEEVATCVGRNGYPIPQVIWYKNGR
    PLKEEKNRVHIQSSQTVE-SSGLYTLQSILKAQLVKEDKDAQFYCELNYRLPSGNHMKES
                                            EDNVFEAPTLVKVFKQPSKPEI-VNKAPF-LETDQLKKLGDCISRDSYPDGNITWYRNGK
                                                                                                                          EKPDGSPVFIAFRSSTKKSVQYDDVPEYKDRLSLSE-NYTLSIANAKISDEKREVCMLVT
                                                                                                                                                                                                       RLVFCLLISAAVLRPGLGWY------TVNSAYGDTIVMPCRLDVPQ-NLMFGKWKY
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90; IG_MHC;
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IG-LIKE C2-TYPE I
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CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                       Score 488.5; DB 1;
Pred. No. 4.4e-25;
2; Mismatches 274;
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                                                                                                                                                                                                                                                                                                                                                                                                                            D (GLCNAC...) (PO)
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CD166 ANTIGEN HOMOLOG PRECURSOR (NEUROLIN) (DM-GRASP
Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C166
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Cypriniformes; Cyprinidae; Cyprininae; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94299040; PubMed=8026643;
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                                                                  TISSUE SPECIFICITY: PRESENT ON ALL RETINAL GANGLION CELLS AND THEIR AXONS (IN EMBRYO). ABSENT FROM MATURE AXONS ALO OF THEIR LENGTH, BUT IS PRESENT ON NEW AND GROWING AXONS FROM THE RGCS AT THE RETINAL MARGIN. REMAINS ON ADULT RGC CELL-CELL COMPACT SITES AND IS CONTINUOUSLY FOUND IN THE AXON TERMINAL ARBOR LAYERS OF THE ADULT TECTUM.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CO 3 C2-LIKE AND 2 V-LIKE DOMAINS.
                                                                                                                                                                                                                                           FUNCTION: CELL ADHESION MOLECULE. INVOLVED IN NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERASUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: PRESENT ON ALL RETINAL GAN TRANSPORTER OF THE PROPERTY OF THE PROPERTY AND THE PROPER
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                                                                FL-DYSLTPTGKYLKNYGENLIYSLDKNASSEAKYTWTKD--NRKLDKLP--DFSKLTYS
                                                                                       YVSDVRVSPAAPE-ROEGSSLTLTCEAESSQDLEFQWLREETGQVLERGPVLQLHDLKRE
                                                                                                                            FSISKQNPSTREAEEETTNDNGVLVLEPARKEHSGRYECQGLDLDTMISLLSEPQELLVN
                                                                                                                                                          --TAKHVMGPDQVSEPESFPIHYPTEKVSLQVVSQSPIREGEDVTLKCQADGNPPPTSFN
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RPTISWNVNGTASEQDQDPQRVLSTLNVLVTPELLETGVECTASNDLGKNTSILFLELVN
                                            AGGGYRCVASVPSIPGLNRTQLVNVAIFGPPWMA--FKERKVWVKENMVLNLSCEASGHP
                                                                                                                                                                                                       ADLIWKKNNQTLVDDGKTIIITSTITKDKITGLSSTSSRLQYTARKEDVESQFTC----
                                                                                                                                                                                                                             PQVIWYKNGRPLKEEKNRVHIQSSQTVES-SGLYTLQSILKAQLVKEDKDAQFYCELNYR
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CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE DOMAIN.

IG-LIKE V-TYPE DOMAIN.
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EMBL; L25057; AAA50048.1; -
HSSP; Q13740; IXVC.
ZFIN; ZDB-GENE-990415-30; C
INTERPRO; IPR000495; -
INTERPRO; IPR003006; -
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"Molecular characterization of fish neurolin: a growth-associated
cell surface protein and member of the immunoglobulin superfamily
the fish retinotectal system with similarities to chick protein
DM-GRASP/SC-1/BEN.";
DM-GRASP/SC-1/BEN.";
-1- FUNCTION: CELL ADHESION MOLECULE. INVOLVED IN NEURITE EXTENSIC
NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        **Ranki J.P., Chang S., Kuwada J.Y.;

"The molecular cloning and characterization DM-GRASP homologs in zebrafish and mouse.";

J. Neurobiol. 25:831-845(1994).
                                                                                                                                                     SIGNAL
                                                                                                                                                                                              PROSITE; PS002
Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                            Signal.
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MEDLINE=94376084; PubMed=8089660;
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Bukaryota; Metazoa; Chordata; Craniata;
Actinopterygii, Teleostei;
Cypriniformes; Cyprinidae; Rasborinae;
                                                                                                                                                                                                                                         PFAM; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94299040; PubMed=8026643;
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AAA50048.1;
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CYTOPLASMIC (POTENTIAL).
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IG-LIKE V-TYPE DOMAIN.
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                                                                                                        HOMOLOG. (POTENTIAL)
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Q1-FEB-1995 (Rel. :

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. 31, Last sequence update)
. 38, Last annotation update)
C-ROUGHEST PROTEIN PRECURSOR
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EMBL; Z21641; CAA79756
EMBL; L11040; AAA16633
PIR; A49448; A49448.
PIR; S34129; S34129.
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Ramos R.G., Igloi G.L., Lichte B., Baumann U., Maier D.,
Schneider T., Brandstaetter J.H., Froehlich A., Fischbach
"The irregular chiasm C-roughest locus of Drosophila, whic
axonal projections and programmed cell death, encodes a no
immunoglobulin-like protein.";
Genes Dev. 7.2533-2547(1993).
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Ephydroidea; Drosophilidae; Drosophila.
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FLYBASE; FBgn0003285; rst.
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TISSUE SPECIFICITY: POSTEMBRYONIC EXPRESSION IS STRONG IN T
DEVELOPING OPTIC LOBE AND IN THE EYE IMAGINAL DISC.
DEVELOPMENTAL STACE: STRONGLY EXPRESSED IN EMBRYOS. ALSO FO
IN LATE LARVAL AND PUPAL STAGES.
SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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FOR PROGRAMMED CELL DEATH I
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IG-LIKE C2-TYPE DOMAIN.
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 EPEEVATCVGRNGYPIPQVIWYKN-GR--
                                                                        VGARVTLPCRVINKQGTLQWTKDDFGLGTSRDLSGFERYAMVGSDEEGDY
                                                 ATLALTQVTPQDERIFLCQGK----
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137; Conser
                        -SLDIYPVMLDDDARYQCQVSPGPEGQPAIRSTFAGLTVLVPPEAPKITQGDVIYATADR
                                                                                                                          Conservative
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20.7%;
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                                                                                                                      Score 270; DB
Pred. No. 1.8e
89; Mismatches
                                                 RPRSQEYRIQLRVYKAPEEPNIQVNPLGIPVNSK 153
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No. 1.
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MEDLINE=91271300; PubMed=1711213;
Chou Y.-H., Hayman M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
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                                                                                        PYOC. Natl. Acad. Sci. U.S.A. 88:4897-4901(1991).

1- FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLEC
THE CATALYTIC ACTIVITY OF TYROSINE KINASE.

1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

1- TISSUE SPECIFICITY: EXPRESSED IN BONE MARROW, STRYMUS AND BRAIN. WEAKLY EXPRESSED IN FIBROBLAS
IN EMBRYONIC LIVER.

1- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-7

1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              645
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; IPR001245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M63437; AAA48933.1;
                                                                                                                                                                                                                                                                                                                        68
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WWERNQERVPTAGRVYQEAEQLVF--TSITEADAGIYTCHAANKA
                                                  IWYKN-----
                                                                                                                                                                                                                                                                                                                                                                 KQPA-SAAEIQPSSTVVLRC
                                                                                                                                                                              TKNEEAMFDCQFAAVPPPTQEWLFEDSPITNRSKTTVFANGSLLITQVKARSTGVYKCIG
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                                                                                                                                                                                                                                                                    KERTLTLR----GAGPDDNGLYYCSARPRAYGSVCSQDNFTLNIIDESFPQAVVYPEDLIV
                                                                                                                                                                                                                                                                                                                   EKRTLIFRVROGOGOSEPGEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                      GRPLKEEKNRVHIQSSQTVESSGLYTLQSILKAQLVKEDKDAQFYCEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 68
                                                                                                                                APEEPNIQVNPLGIPVNSKEPEEVATCVGRNGYPIPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
N-LINKED (GLCN#)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG-LIKE C2-TYPE DOMAIN 1
IG-LIKE C2-TYPE DOMAIN 2
IG-LIKE C2-TYPE DOMAIN 3
IG-LIKE C2-TYPE DOMAIN 3
IG-LIKE C2-TYPE DOMAIN 5
IG-LIKE C2-TYPE DOMAIN 5
IG-LIKE C2-TYPE DOMAIN 6
IG-LIKE C2-TYPE DOMAIN 6
IG-LIKE C2-TYPE DOMAIN 7
IG-LIKE C2-TYPE DOMAIN 7
IG-LIKE C2-TYPE DOMAIN 7
IG-LIKE C2-TYPE DOMAIN 7
IG-LIKE C3-TYPE DOMAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 259.5;
Pred. No. 1.4e
99; Mismatches
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CYTOPLASMIC
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LINKED (GLCNAC...
LINKED (GLCNAC...
1752442AEA4CB702 (
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CYTOPIASHIA:

(NCAM).";

molecule (NCAM).";

Nucleic Acids Res. 17:10321-10335(1989).

-I- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE

-I- FUNCTION: ADHESION, NEURITE FASCICULATION, OUT(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCA1_XENLA
P16170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180)
                  between
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=90098871; PubMed=2481269;

Krieg P.A., Sakaguchi D.S., Kintner C.R.;

"Primary structure and developmental expression of a l
cytoplasmic domain form of Xenopus laevis neural cell
                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                561
                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESU
   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                    SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                               DEVELOPMENTAL STAGE: THE MRNA ENCODI
TRANSCRIPT PRESENT IN BOTH MATERNAL
EARLY NEURAL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYRLPSGNHMKESREVTVPVFYPTEKVWLEVEPVGMLKEGDRVEIRCLADGNPPPHFSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEASGHPRPTISWNVNGTASEODODPQRVLSTLNVLVTPELLETGVECTASNDLGKNTSI
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Matches 155
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INTERPRO; IPRO01777; -.
INTERPRO; IPRO03006; -.
PFAM; PF00041; fn3; 2.
PFAM; PF00047; fg; 5.
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CARBOHYD
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entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                               PELVEVEVGSTALLKCGLSQSQGNLSHVDWFSVHKEKRTLIFRVRQGQGQSEPGEYEQRL 92
                                                                                       NGRPLKEEKNRVHIQSSQTVESSGLYTLQSILKAQLVKEDKDAQFYCELNYRLPSGNHMK
                                                                                                            EGRILARGEINYKDIQVIVNVPPTIQARQLRVNATANMAESVVLSCDADGFPDPEISWLK
                                                                                                                                                      KEGEDAVIICDVSSSIPSIITWRHKGKDVIFKKDVRFVVLANNYLQIRGIKKTDEGTYRC 186
                                                                                                                                                                                                  SVVRSDDYTSTLTIYNASSQDAGIYKCVASNEAEGESEGTVNLKIYQKLTFKNAPTPQEF 126
                                                                                                                                                                                                                     SL---QDRGATLALTQVTPQDERIFLC-----QGK-----
                                                                                                                                                                                                                                           PDQGEISLGESKFFLC---QVSGEATDISWYSPTGEKLVT--
  ETTNDNGVLVLEPARKE-
                                         ESREVTVPVFYPTEKVWLEVEPVGMLKEGDRVEIRCLADGNPPPHFSISKQNPSTREAEE
                        EAEATILLKVYAKPKITYVENKTAV-
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323
420
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                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                       Score 256; DB
Pred. No. 2.5e
00; Mismatches
                                                                                                                                                                                                                                                                                                                                             MISSING (IN ISOFORM N
MW; 62738B55B03F3E83
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PROBABLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOFORM
                         ·ELDEITLTCEASGDPIP - - SITWRTAVRNISSE
    HSGRYEC ---
                                                                  -QSEMTIHHVEKDDEAEYSCIAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL ADHESION MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
   QGLDLDTMISLLSEPQELLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                           Length 1088;
                                                                                                                                                                             -IQLRVYKAPEE---- 138
                                                                                                                                                                                                                                                                                                                                                          N-CAM 140).
                                                                                                                                                                                                                          ----- RPRSQEY 126
                                                                                                                                                                                                                                                                                                                                              CRC64;
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                               -----QQQI 66
                                                                                                                                                                                                                                                                                        336;
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                                                                     -NQAG
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RESULT IDA 2_MM AC POOR REA AC POOR REA AC POOR REA AC REA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _MOUSE
MCA2_MOUSE STANDARD; PRT; 725 AA.
P13594; Q61950;
O1-JAN-1990 (Rel. 13, Created)
O1-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NEURAL CELL ADHESION MOLECULE, PHOSPHATIDYLINOSITOL-LINKED
distinct NCAM (1988)
                                                                                                                                                                                                                                                                                                                                                           "Isolation and nucleotide sequence of mouse NCAM cDNA that a Mr 79,000 polypeptide without a membrane-spanning rows [2]
                                       SEQUENCE OF 642-725 FROM N.A.
MEDLINE-88283628; pubMed=3396534;
Barbas J.A., Chaix J.C., Steinmetz M.,
"Differential splicing and alternative
distinct NCAM transcripts and proteins
                                                                                                                                                                                       SEQUENCE OF 20-700 FROM N.A.
STRAIN-C57BL/6; TISSUE-BRAIN;
MEDLINE-89251563; PubMed-2721486;
Santoni M.J., Barthels D., Vopper G., Boned A.,
"Differential exon usage involving an unusual speciates at least eight types of NCAM cDNA in membo J. 8:385-392(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6;
MEDLINE=87246524; PubMed=3595563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRECURSOR (N-CAM
NCAM1 OR NCAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---EERTPNHDGSNQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSGDKRAPGDQGEKYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKGKLPC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCGLLMCIAVNFCGKAGPGAKGKDIEEGKAAFSKDESK--EPIVEVRTE------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNVLV-TPEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPDSTGGVPILKYKAEWRVIGHEKWHTKYYDAKEVNAESIITVMGLKPETSYMVKLSAMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GHPRPTISWNVN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120) (NCAM-120).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -WMAFKERKVWVK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LETGVE----CTASNDLGKNTSIL--FLELVNLTTLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -RRSGKQEITLPPSRKSELVVEVKSDKLPEEMGLLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                      a membrane-spanning region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GTASE-----
                                            Goridis C.;
polyadenylation
in the mouse.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ENM - - VLNLSCEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muridae;
                                                                                                                                                                                                                splicing mechanism n mouse brain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murinae;
                                                                generates
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PIR; A29673; IJMSNG.
MGD; MGI:97281; NCAM.
INTERREG; IPR001777; -
INTERPRO; IPR003006; -
PFAM; PF000041; fn3; 2.
PFAM; PF000047; ig; 5.
Cell adhesion; Glycoprotein; R
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MEDLINE=86140120;
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                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Structural and immunological characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANC ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS ON-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.

SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEURON-NEURON ADHESION, NEURITE FASCICULATION, NEURITES, ETC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EM
European Bioinformatics Institute. There are no restr
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X15049; CAA33148
X07195; CAA30173
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QD -> KT (IN REF. 2).

T -> K (IN REF. 2).

T -> R (IN REF. 2).

D -> V (IN REF. 2).
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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l; Heparin-binding; GPI-anchor
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Best Local Similarity
Matches 141; Conser

7.3%; nilarity 20.6%; Conservative 9

92;

Score 246.5; DB 1; Pred. No. 6.1e-09; 2; Mismatches 261;

Length 725; Indels

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MEDLINE-92181437; PubMed=1371918;

Hession C., Moy P., Tizard R., Chisholm P., Williams C., Wysk M.,

Hession C., Moy P., Tizard R., Chisholm P., Williams C., Wysk M.,

Burkly L., Miyake K., Kincade P., Lobb R.;

"Cloning of murine and rat vascular cell adhesion molecule-1.";

"Cloning of murine and rat vascular cell adhesion molecule-1.";

Biochem. Blophys. Res. Commun. 183:163-169(1992).

-I- FUNCTION: IMPORTANT IN CELL-CELL ADHESION. INTERACTS WITH THE BETA-1

TN IFFIKOCYTE-ENDOTHELIAL CELL ADHESION. INTERACTS WITH THE BETA-1
                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
VASCULAR CELL ADHESION PROTEIN 1 PRECURSOR (V-CAM VCAMI OR VCAM-1.
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01-APR-1993 (Rel. 25,
30-MAY-2000 (Rel. 39,
                                                                                                                                                               SEQUENCE FROM
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Sciurognathi; Muridae;
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED ON INFLAMED VASCULAR ENDOTHELIUM,
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  LEFQWLREET - -
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Eukaryota; Metazoa;
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01-JAN-1990 (Rel. 13,
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Cell a
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ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS
N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULATION, NEURON-NEURON ADHESION, NEURITE FASCICULATION,
                                                                                                         S00846;
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S.J., Shull G.E., Santoni M
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                                                                                                                                                                                          s requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    the Swiss Institute of Bioinformatics
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FIBRONECTIN TYPE-III.
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HEPARIN-BINDING (POTENT)
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AN NOORAN D.M., HOTIGAN E.A., Ledbetter S.R., Vogeli G., Sasaki M., A Yamada Y., Hassell J.R.;

AY Yamada Y., Hassell J.R.;

AY Tamada Y., Hassell J.R.;

AY "Identification of cDNA clones encoding different domains of the Transport of the Protein the Protein State Protein State Protein State Protein State Protein Office Protein Office Protein State Protein Office Protein State Protein Office Protein State Protein State
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE
PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).
                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                             AND O-LINKED OLIGOSACCHARIDES.
SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV.
SIMILARITY: CONTAINS 15 IAMUNOGLOBULIN-LIKE C2-TYPE DOMAINS SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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Metazoa; Rodentia; S
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e A., Valente P.,
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         INTERPRO; IPRO00082; -.

INTERPRO; IPRO00082; -.

DR INTERPRO; IPRO01488; -.

DR INTERPRO; IPRO01791; -.

R INTERPRO; IPRO01791; -.

R INTERPRO; IPRO02049; -.

R INTERPRO; IPRO020172; -.

PEAM; PE00047; Ig; 15.

PEAM; PE00052; laminin_EGF; 8.

PEAM; PE00053; laminin_EGF; 8.

PEAM; PE00057; Idl_recept_a: '

'INTS; PRO0010; EGFHT'

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PROSITE; PS010022; EGF_1; 8.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01209; LDLRA_1; 4.

PROSITE; PS01248; LAMININ_TYPE_EGF; PROSITE; PS50068; LDLRA_2; 4.
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LDL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 2.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

IG-LIKE C2-TYPE DOMAIN 1.

LAMININ DOMAIN IV 1 (DOMAIN III A).

LAMININ EGF-LIKE 1 (C-TERMINAL).

LAMININ EGF-LIKE 2.

LAMININ EGF-LIKE 3

LAMININ EGF-LIKE 5 (N-TERMINAL).

LAMININ EGF-LIKE 5 (N-TERMINAL).

LAMININ EGF-LIKE 5 (C-TERMINAL).

LAMININ EGF-LIKE 5 (C-TERMINAL).

LAMININ EGF-LIKE 5 (C-TERMINAL).

LAMININ EGF-LIKE 6 (C-TERMINAL).

LAMININ EGF-LIKE 9 (N-TERMINAL).
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DOMAIN IIA (1 IGG-REPEAT)
DOMAIN III (SIMILAR TO SHORT
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N EGF-LIKE 10
N EGF-LIKE 11
E C2-TYPE DOM
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RESULT I. PGBM_MOUSE
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ID PGBM_M
AC 005793
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MEDLINE-89034110; SEQUENCE OF 940-1601 molecule. chain, sulfate MEDLINE=92078153; pubMec Noonan D.M., Fulle A., V Yamada Y., Hassell J.R.;

TISSUE-MELANOMA

Eukaryota; Metazoa; Mammalia; Eutheria; EQUENCE FROM N.A.

musculus

This SWI

M77174; J04054; J04055; P01130;

AAA39899.

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22.3%;
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                                     Score 244.5;
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O-TINK
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EGF-LIKE 2.
LAMININ G-LIKE 2
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HEPARAN SULFATE (
HEPARAN SULFATE (
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(GLYCOSAMINOGLYCAN)
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NCA1_BOVIN
                                                                                                                                                                                   TISSUE-BRAIN CORTEX;

MEDILIND-89378239; PubMed=2776887;

Lipkin V.M., Khramtsov N.V., Andreeva S.G., Moshnyakov M.V.,

Petukhova G.V., Rakitina T.V., Feshchenko E.A., Ishchenko K.

Mirzoeva S.F., Chernova M.N., Dranytsyna S.M.;

"Calmodulin-independent bovine brain adenylate cyclase. Amil sequence and nucleotide sequence of the corresponding cDNA."

FEBS Lett. 254:69-73(1989).
                                                                                                                                                                                                                                                                                                                                                                                                      P31836;
Ol-JUL-1993 (Rel. 26, Created)
Ol-JUL-1993 (Rel. 26, Last sequence
15-JUL-1999 (Rel. 38, Last annotati
NEURAL CELL ADHESION MOLECULE, 140
adenylyl cyclase has
molecules (N-CAMs).";
                                                    IDENTIFICATION AS MEDLINE-92111748;
                                                                                       MEDLINE=86140120; PubMed=3512556; Rougon G., Marshak D.R.; Rougon G., Marshak D.R.; "Structureal and immunological characterization of the domain of mammalian neural cell adhesion molecules.", J. Biol. Chem. 261:3396-3401(1986).
                                       Premont R.T.;
                                                                                                                                              MEDLINE-86140120;
                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartiod
                        "A bovine brain cDNA
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL
                                                                                                                                                                                                                                                                                                                                Bovidae;
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NCAM1 OR NCAM
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26, Last sequence update)
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38, Last annotation update)
140 KDA ISOFORM PRECURSOR (N-CAM 140)
                                                    N-CAM.
PubMed=1765159;
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                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Eutel Cetartiodactyla; Ruminantia; Pecora;
          purported to encode calmodulin-insensitive extensive identity with neural cell adhesi
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                                                                                                                      amino-terminal
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          adhesion
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HSSP; PA0189; 1BQU
INTERPRO; IPR001777; -
INTERPRO; IPR003006; -
INTERPRO; IPR003006; -
PFAM; PF00047; 19; 5
PFAM; PF00047; 19; 5
Cell adhesion; Glycoprote
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-i- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.

-i- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-i- SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
-I- LAUTION: WAS ORIGINALLY (REF. 1) THOUGHT TO BE A CALMODULIN-INDEPENDENT ADENYLATE CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
DOMAIN
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APTPQEEREGEDAVIVCDVVSSLP-PTIIWKHKGRDVILKKDVRFIVLTNNYLQIRG---
                                                                                                                              RLSL---QDRGATLALTQVTPQDERIFLC--QGKRPRSQEYRIQLRVYKAPEEPNIQVNP
                                                                                                                                                                               PSQGEISVGESKFFLC---QVAGDAKDKDISWFSPNGEKLT---
                                                                                    RISVVWNDDSSSTLTIYNANIDDAGIYKCVVTAEDGTESEATVNVKIFQ-----KLMFKN 122
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HEPARIN BINDING (POTENTIAL).

BY SIMILARITY.

BY
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EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN.

IG-LIKE C2-TYPE TOMAIN.

IG-LIKE C2-TYPE TOMAIN.

IG-LIKE C2-TYPE TOMAIN.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.
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Pred. No. 1.4e-08;
3; Mismatches 245;
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Search completed: March 23, 2001, 12:31:56 Job time: $74 \ \text{sec}$

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ALIGNMENTS

RESULT 1 OPS812 PRELIMINARY; PRT; 646 AA. OPS812; PRELIMINARY; PRT; 646 AA. OPS812; PREMBLEL 10, Created) OPS812; Calculation update) OO -MAY-1999 (TrEMBLEL 113, Last sequence update) OO -MAY-1999 (TREMBLEL 113, Last sequence update) OO OPS812; Calculation update) OO OPS812; Ca

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STRAIN-H.B190V+; TISSUE-THYMUS;
MEDLINE-97133433; PubMed-8978830;
Wainio O., Dunon D., Aissi F., Dangy J.P., McNagny
"HEMCAM, an adhesion molecule expressed by c-kit+ h
progenitors.";
                                                                                                                                                                                                                                                                                                                                      HEMCAM PRECURSOR.

Gallus gallus (Chicken).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                            SEQUENCE
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BL; Y08855; CAA70080.1; -.
TERPRO; IPRO03006; -.
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                     RRP-----LRSGEAVRHHASGVRIDETEYSERLSVGEDKA-LSISKVTRQDNARTFICQ
                                          KEKRTLIFRVRQGQG-----
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                                        -QSEPGEYEQRLSLQDRGATLALTQVTPQDE-RIFLCQ 117
                                                                                                      Score 1104; D
Pred. No. 6.3e
16; Mismatches
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5.3e-78;
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                                                                                    GRSGKQDITKPEARKDKNVVEVKSDKLSEEAGLLQGANGEKRSPADQSEKYIDLRN
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Best Local Similarity
Matches 248; Conserv
                                                                                                                               Taira E., Nagino T., Taniura H., Takaha N.,
Higuchi H., Miki N.;
"Expression and functional analysis of a no
immunoglobulin superfamily cell adhesion mo
J. Biol. Chem. 270:28681-28687(1995).
EMBL; D49849; BAA08648.1;
INTERPRO; IPRO03006; -.
PFAM; PF00047; ig: 5.
SEQUENCE 626 AA; 69074 MW; C4791EEC2EC5
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Eukaryota; Metazoa; Chor
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01-NOV-1996 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
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                                        CAFLLAACCCCPRVAGVPGEAEQPAPELVEVEVGSTALLKCGL----SQSQGNLSHVDW
FSVHKEKRTLIFR---
                                                                      30.5%; Silarity 37.4%; P
Conservative 114;
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Pred. No. 9.4e:
14; Mismatches
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; Galliformes; Phasianidae; Phasiani
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QSEPGEYEQRLSLQDRGATLALTQVTPQDE
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J. Cell Biol. 135:1655-1668(1996)
EMBL; Y08856; CAA70081.1; -.
INTERPRO; IPRO03006; -.
PFAM; PF00047; ig; 5.
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SIGNAL
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STRAIN=H.B19OV+; TISSUE-THYMUS;
MEDLINE-97133433; PubMed-8978830;
Vainio O., Dunon D., Aissi F., Da
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Archosauria; Aves; Neognathae;
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01-NOV-1996 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
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                    SEQUENCE FROM N.A.
STRALN=LEGORN; TISSUE=GIZZARD;
STRALN=LE94213753; PubMed=8161457;
MEDLINE=94213753; PubMed=8161457;
Taira E., Takaha N., Taniura H., Kim C., Miki N.;
"Molecular cloning and functional expression of g
adhesion molecule that binds to neurite outgrowth
Neuron 12:861-872(1994).
                                                                                                                                  Eukaryota; Metazoa;
Archosauria; Aves; J
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAPERQEGSSLILITCEAESSQDLEFQWLREETGQVLERGPVLQLHDLKREAGGGYRCVAS::| | | | : | | : | : | | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAEEETINDNGVLVLEPARKEHSGRYECQGLDLDTMISLLSEPQELLVNYVSDVRV--SP
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                                                                                                                                                                                                                                                                                                                                                                                                    SEQDQDPQRVLSTLNVLVTPELLETGVECTASNDLGKNTSILFLELVNLTTLTPDSNTTT
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                                                                                                                                                           gallus (Chicken)
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                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                      578
                                                                                                                                     ; Chordata;
Neognathae;
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Pred. No. 7.7e
109; Mismatches
                                                                                                                                                                                Created)
Last sequence Last annotation
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                                                                                                                                      Craniata; Ver; Galliformes;
                                                                                                                                                                                                                              PRT;
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annotation
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7.7e-65;
hes 213;
                                 ssion of gicerin,
outgrowth factor
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nes; Phasianidae;
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Q98923 PRELIMINANI,
Q98923;
Q98923;
Q1-FEB-1997 (TrEMBLrel. 02, Creat
O1-FEB-1997 (TrEMBLrel. 12, Last
O1-MAY-2000 (TrEMBLrel. 13, Last
E HEMCAM PRECURSOR.
S Gallus gallus (Chicken)
S Gallus gallus (Chicken)
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Best Local Similarity
Matches 216; Conserv
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Cell adhesion; Extracellular matrix
SEQUENCE 584 AA; 64378 MW; 876E0C3E920BA92F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Expression and functional analysis of a immunoglobulin superfamily cell adhesion J. Blol. Chem. 270:28681-28687(1995).
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MEDLINE-96081930;
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                                                                                                                                                                                                                                                                                                     GYRCVASVPSIPGLNRTQLVNVAIFGPPWMAFKERKVWVKENMVLNLSCEASGHPRPTIS
                                                                                                                                                                                                                                                                                                                                          VRV--SPAAPERQEGSSLTLTCEAESSQDLEFQWLREETGQVLERGPVLQLHDLKREAGG
                                                                                                                                                                                                                                                                                                                                                                        ELGDSWQDMTSLADTNDGVLMLHNVSKSSSGLYRCQTLDLDDMTQHEGD-VELVVNYIEG
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                                                                                                                                                                                                                                                                                                                              VQVKMEPSSP-LHEGDSVRLSCTAHSPVKLDYQW-RDARGRKVAEGNQLLLTNLTFETSS
                                                                                                                                                                                                                                                                                                                                                                                                                      LQGQMRTKDSPRVNVTVFYPTEHVELRVATNAGIVKEGDDVKLVCDADGNPAPVFSFFRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPNITWYKNGEPLLQEEDKTKILTTLVRESNGLYTVVSTLFSKVTREDRNSLFHCTVHYW
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0; PubMed=7499388;
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                                    , Created)
, Last sequence up
, Last annotation
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Pred. No. 3.9e-59;
7; Mismatches 210
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     Craniata;
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    Vertebrata;
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molecule.";
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     Euteleostomi;
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Best Local
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Matches 172; Conserv
           SEQUENCE FROM
STRAIN=129/SV;
                                                                                         01-OCT-2000 (TrembLrel.
01-OCT-2000 (TrembLrel.
01-OCT-2000 (TrembLrel.
LUTHERAN GLYCOPROTEIN.
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SIGNAL
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01-OCT-2000
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SEQUENCE
                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                             NCBI_TaxID=10090;
                                                                                                                                                     Q9JКВ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN+H.B190V+; TISSUE=THYMUS;
MEDLINE=97133433; PubMed=8978830;
Wainio O., Dunon D., Aissi F., Dangy J.P., McNagny K.M., Imhof
"HEMCAM, an adhesion molecule expressed by c-kit+ hemopoietic
progenitors.";
J. Cell B101. 135:1655-1668(1996).
EMBL; Y08884; CAA70079.1; -.
ENBL; TO8897; CAA70079.1; -.
INTERPRO; IPR003006; -.
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 G
                                                                              musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CPFLCLLLCC-----GAAGRLEVYMPAVLEVEIGSTARLECSFSIPGNASFTSIEWFYVN 76
                                                                                                                                                                                                                      VPSIPGLNRTQLVNVAIFGPPWMAFKERKVWVKENWVLNLSCEASGHPRPTISWNVNGT
                                                                                                                                                                                                                                                                  \tt ARSVPGLEQSKQVAVAVKGKPRIVALSAPLYVRQDEVINLTCKAIAFPQPSFHWSINGT
                                                                                                                                                                                                                                                      SSP-LHEGDSVRLSCTAHSPVKLDYQW-RDARGRKVAEGNQLLLINLTFETSSNFSCRVK 426
                                                                                                                                                                                                                                                                                                    DMTSLADTNDGVLMLHNVSKSSSGLYRCQTLDLDDMTQHEGD-VELVVNYIEGVQVKMEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEKRTLIFRVRQGQG------QSEPGEYEQRLSLQDRGATLALTQVTPQDE-RIFLCQ 117
                                                                                                                                                                                                                                                                                                                                             KDSPRVNVTVFYPTEHVELRVATNAGIVKEGDDVKLVCDADGNPAPVFSFFRRELGDSWQ
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504. AA;
                                                                                                                                                   PRELIMINARY;
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T.-N.,
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504
55540
                                                         Chordata;
Rodentia;
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Last seq
Last ann
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Pred. No. 3.7e-50;
1; Mismatches 184
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                                                    Craniata; Vert
Sciurognathi;
                                                                                                                                                   PRT;
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                                                                                                    sequence update)
annotation update)
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                                                        Vertebrata;
thi; Muridae;
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                                                      Euteleostomi;
Murinae; Mus
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RESULT Q9R069 ID Q9R070 Q9R070
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Best Local
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                                                                                                                        Q9R069 PRELIMINARY;
Q9R069;
01-MAY-2000 (TrEMBLrel. 13, 0
01-MAY-2000 (TrEMBLrel. 13, I
01-OCT-2000 (TrEMBLrel. 15, I
LUTHERAN GLYCOPROTEIN.
                         Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                 GPLU
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"Mouse Lutheran Glycoprotein Gene.";
"Mouse (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF246667; AAF61742.1;
"SEQUENCE 622 AA; 67543 MW; 3A877738D96F6CD9 CRC64;
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                                                                                                 OR LU.
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                                                                                                                                                                                                                                                                                                                                                                         RGGSGFGDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVLGAVLYFLYKKGKLPCRRSGKQEITLPPSRKSELVVEVKSDKLPEEMGLLQG--SSGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAGGGYRCVASVPSIPGLNRTQLVNVAIFGPPWM----AFKERKVWVKENMYLNLSCEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPLELS - - APEELFVFLNSSSTVVNCSARGLPTPTVRWTKDSV - - TLADGPMLSLQSVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDVRVSPAAPER----QEGSSLTLTCEAESSQDLEFQWLREETGQVLERGPVLQLHDLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQQ-GTQE-EQLNVNLKGNLTLEGVHRNQSGIYGCRVEDYDADEEVQLVKK-LKLHVAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQNPSTREAEEETTNDNGVLVLEPARKEHSGRYEC--QGLDLDTMISLLSEPQELLVNYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGNHMK-ESREVTVPVFYPTEKV--WLEVEPV--GMLKEGDRVEIRCLADGNPPPHFSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WYKNGRPLK---EEKNRVHIQSSQTVESSGLYTLQSILKAQLVKEDKDAQFYCELNYRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CVVKAGAAGTSEATSSVRVFATPEDTEVSPNKGTLSVMDQFAQEIATCSSNNGNPVPRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGARHRLASVEPQGSEFLGTV-HSLGRVPPYEVDSR-----GRLVIAKVQVGDGRDYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGHPRPTISWNVNGTASEQDQDPQR--VLSTLNVLVTPELLETGVECTASNDLGKNTSIL
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91; Conservative
  s (Mouse).
Metazoa; Chordata; C
--+heria; Rodentia;
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                                                                                                                                               Last sequence up
Last annotation
                                                                                                                                                                                                  Created)
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                         Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                622
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                                                                                                                                                                                                                                              AA
                                                                                                                                            update)
on update)
                            Muridae;
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                         Murinae;
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Best Local Similarity
Matches 190; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mouse Lutheran glycoprotein.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AF109160; AAF14226-1; -
EMBL; AF221507; AAF34657.1; -
INTERPRO; IFR003006; -
PFAM; PF00047; ig; 5.
SEQUENCE 622 AA; 67670 MW; 257903F08D47EB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Rahuel C., Colin Y., Goossens D.
Le Van Kim C.;
"Characterization of a mouse lam
human blood group Lutheran gene.
nmunogenetics 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM
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                       KRAPGDQGEK
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RGGSGGFGDE
                                               LLVVAAFYCMRRKGRPGCCR--RAEKGAPPAREPEL--SHSGSERPEHTGLLMGGPSGGG
                                                                    AVLGAVLYFLYKKGKLPCRRSGKQEITLPPSRKSELVVEVKSDKLPEEMGLLQG-
                                                                                                                      FLELVNLTTLTPDSNTTTGLSTSTASPHTRANSTSTERKLPEPESRGVVIVAVIVCILVL
                                                                                                                                             RGFPEPKLTWSQRGDTPAEPPFEGRGWKSSSLMVKVTSALSREGVSCEASNIHGKKGHVF
                                                                                                                                                                 SGHPRPTISWNVNGTASEQDQDPQR--VLSTLNVLVTPELLETGVECTASNDLGKNTSIL
                                                                                                                                                                                              DSAGTYTCEASTPTVPLLSRTQSFQLIVQGAPELKPNEIMPKSGNSWTEGDEVM-LTCSA
                                                                                                                                                                                                         EAGGGYRCVASVPSIPGLNRTQLVNVAIFGPPWM-----AFKERKVWVKENMVLNLSCEA
                                                                                                                                                                                                                                             DPLELS - - VPEELFVFLNSSSTVVNCSARGLPTPTVRWTKDSV - - TLADGPMLSLQSVTF
                                                                                                                                                                                                                                                                    SDVRVSPAAPER----QEGSSLTLTCEAESSQDLEFQWLREETGQVLERGPVLQLHDLKR
                                                                                                                                                                                                                                                                                                           SGQHGRLDSHTFRLTLHYPTEHVEFWVGSPSTTEGWVREGDAVQLLCQGDGSPSPEYSFF
                                                                                                                                                                                                                                                                                                                                                            SGNHMK-ESREVTVPVFYPTEKV--WLEVEPV--GMLKEGDRVEIRCLADGNPPPHFSIS
                                                                                                                                                                                                                                                                                                                                                                                            WYRNGQRLEVPMEVNQKGYITIRTVREASGLYSLTSTLYLRLHKDDRDANFHCAAHYDLP
                                                                                                                                                                                                                                                                                                                                                                                                                    WYKNGRPLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CQGK--RPRSQEYRIQLRVYKAPEEPNIQVNPLGIPVNSKEPEEVATCVGRNGYPIPQVI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGARHRLASVEPQGSEFLGTV-HSLGRVPPYEVDSR-----GRLVIAKVQVGDGRDYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLLSG-----YSGAQAELHVSVPPRVEVMRGEQVALDC---TPREHPEHYVLEWFLVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLLAACCCCPRVAGVPGEAEQPAPELVEVEVGSTALLKCGLSQSQGNLSH--VDWF----
                                                                                                                                                                                                                                                                                             RQQ-GTQE-EQLNVNLKGNLTLERVHRNQSGIYGCRVEDYDADEEVQLVKK-LKLHVAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 102;
621
                       640
                                                                                                                                                                                                                                                                                                                                                                                                            -EEKNRVHIQSSQTVESSGLYTLQSILKAQLVKEDKDAQFYCELNYRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 614; DB
Pred. No. 1.3e-
02; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laminin
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.3e-39;
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RESULT

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O35112 PRELIMINA...,

O35112; O55172;

O1-JUN-1998 (TremBLrel. 06, Created)

O1-JUN-1998 (TremBLrel. 06, Last sequence update)

O1-MAY-2000 (TremBLrel. 13, Last annotation update)

O1-MAY-2000 (TremBLrel. 13, Last annotation update)

CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE)

(ALCAM) (MEMD PROTEIN) (HB2) (KG-CAM).
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DISULFID
DISULFID
                                                                                                                                               Signal;
SIGNAL
                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  differentiation.";
T. Bone Miner. Res. 13:655-663(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                        PFAM; PF00047; ig; 5.
Cell adhesion; Immunoglobulin
                                                                                                                                                                                                                                                                                                             Brain Res. 640:296-307(1994).
                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 29-38.
MEDLINE-942772944; PubMed-8004458;
Peduzzī J.D., Irwin M.H., Geisert
"Distribution and characteristics
                                                                                                                                                                                                                                                                                                                                                                                                                            Bruder S.P., Ricalton N.S., Boynton R.E.,
Zaia J., Barry F.P.;
                                                                           TRANSMEN
                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                  rat
                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-MESENCHYME; MEDLINE-98215351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and characterization of HB2, a candidate high lipoprotein receptor. Sequence homology with members of immunoglobulin superfamily of membrane proteins."; J. Biol. Chem. 272:16778-16782(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fidge N.;
                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                          "Mesenchymal stem cell surface antigen
leukocyte cell adhesion molecule and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 270-361 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsumoto A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL S
MEDLINE-97347476; PubMed-9201982;
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                                                                                                                                          INTERPRO; IPR003006; -.
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Antigen.
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438
D 433
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583
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548
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120
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227
227
329
492
113
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        POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE DOMAIN.

IG-LIKE V-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.

POTENTIAL.
                                                                                             POTENTIAL.
CD166 ANTIGEN
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Sciurognathi;
 POTENTIAL.
                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                        domain;
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                                                                                                                         Glycoprotein;
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90 kDa protein,
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                                                                                                                                                                                                                                                                                                                                                                                                           involved in osteogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muridae;
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                                                                                                                         Transmembrane;
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; Murinae; Rattus
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RESULT 046634

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046634; 01-JUN-1998 01-JUN-1998 01-MAY-2000

(TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 13, Last annotation update)

CD166 ANTIGEN (FRAGMENT).

(ACTIVATED

LEUKOCYTE-CELL

ADHESION MOLECULE) (ALCAM)

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CONFLICT
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SEQUENCE
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KTASKHVNKDLGNMEENKKLE
                    KLPCRRSGKQEITLPPSRKSE
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                                                                                                                                                                     TKQIGDTLPVSCTISASRNATVVWMKDNIR--LRSSP--SFSSLHYQDAGNYVCETALQE
                                                                                                                                                                                                                                                                                                                                                                                                                                          RLYCAFILAACCCCPRVAGVPGEAEQPAPELVEVEVGSTALLKCGLSQSQGNLSHVDWFS
                                                                                  NQTEESPYINGRYYS--KIIISPEENVT-LTCTAENQLERTVNSLNVSAISI----PE--
                                                                                             VEGLKKRESLTLIVEGKP--QIKMTKKTDPSGLSKTIICHVEGFPKPAIQWTITGSGSVI
                                                                                                                                                                                                                                 EEETTNDNGVLVLEPARKEHSGRYECQGLDLDTMISLLSEPQELLVNYVSDVRVSPAAP-
                                                                                                                                                                                                                                                                                                VLQPVDGEVSILFKKEIDPGTQLYTMTSSLEYKTTKSDIQMPFTCSVTYYGPSGQKTIYS
                                                                                                                                                                                                                                                                                                                     PLKEEKNRVHIQSSQTVE-SSGLYTLQSILKAQLVKEDKDAQFYCELNYRLPSGNHMKES
                                                                                                                                                                                                                                                                                                                                                              RPRSQEYRIQLRVYKAPEEPNIQVNPLGIPVNSKEPEEVATCVGRNGYPIPQVIWYKNGR
                                                                                                                                                                                                                                                                                                                                                                                    EKPDGSPVFIAFRSSTKKSVQYDDVPEYKDRLSLSE-NYTLSINNAKISDEKRFVCMLVT
                                                                                                                                                                                                                                                                                                                                                                                                      VHKEKRTLIFRVRQGQGQS-----EPGEYEQRLSLQDRGATLALTQVTPQDERIFLCQ-GK
                                                             TTTGLSTSTASPHTRANSTSTERKLPEPESRGVVIVAVIVCILVLAVLGAVLYFLY-KKG
                                                                                                                                                                                        ERQEGSSLTLTCEAESSQDLEFQWLREETGQVLERGPVLQLHDLKREAGGGYRCVASVPS
                                                                                                                                                                                                             NTYTLTD-----VRRNATGDYKCSLIDQRNMAASTT----ITVHYL-DLSLNPSGEV
                                                                                                                                                                                                                                                                           REVTVPVFYPTEKVWLEV-EPVGMLKEGDRVEIRCLADGNPPPH---FSISKQNPSTREA
                                                                                                                                                                                                                                                                                                                                          EDNVFEAPTLVKVFKQPSKPEI-VNRAAF-LETEQLKKLGDCISRDSYPDGNITWYRNGK
                                                                                                                                                                                                                                                                                                                                                                                                                             RLVFCLLISAAVLRPGLGWY---
                                                                                                                                                                                                                                                       EQAIFDIYYPTEQVTIQVLPPKNAIKEGDNTTLQCLGNGNPPPEEFMFYLPGQAEGIRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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354
435
339
367
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480
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                                         HDEADDISDENR-EKVNDQAKLIVGIVVGLLLAALVAGVVYWLYMKKS
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392
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351
167
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480
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575
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D36B73854F5DF61E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e 499.5; L. No. 1e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73;
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Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=MESENCHYME;
MEDLINE=98215351;
                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
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DOMAIN
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Cell adhesion; Immunoglobulin
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 193
                                                                                                                 146
                       258
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                                                                                                                                        23
                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bone Miner. Res. 13:655-663(1998).

FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF TAND B CELLS TACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS THE NERVOUS SYSTEM. MAY BE INVOLVED IN OSTEOGRESSIS. MAY PLAY A IMPORTANT ROLE IN THE DEVELOPMENT OF A VARIETY OF MESENCHYMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUES (BY SIMILARITY).
SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAIN
C2-LIKE AND 2 V-LIKE DOMAINS.
                                                         LGIPVNSKEP----
                                                                                                                                                              EYEQRLSLQDRGATLALTQVTPQDERIFLCQ-GKRPRSQEYRIQLRVYKAPEEPNIQVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y13242; CAA73694.1;
Q13740; 1KJC.
PSKTAIKEGDIITLKCLGNGNPPPEEFLFYLPGQPEGIRSSNTYTLTD-
                       P-VGMLKEGDRVEIRCLADGNPPPH----FSISKQNPSTREAEEETTNDNGVLVLEPARKE 313
                                             VTQLYTMTSSLEYKATKADIQMQFTCSVTYYGPSGQKTVQSEQAIFDIYYPTEQVTIQVL
                                                                                                                                        EYEDRLSLSE-NYTLSISNARISDEKRFVCMLVTEDNVFEAPTIVKVFKQPSKPEIV---
                                                                                                                                                                                  al Similarity
143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.P., Ricalton N.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barry F.P.;
                                                                                          -SKAPFLETEQLKKLGDCISKDSYPDGNITWYRNGKVLQPLEGVVVLIFKKQMDP
                                                                                                                                                                                                                                            418
437
521
                                                                                                                                                                                                                                                                                                                                                                                                                                467
467
488
488
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9556065
                                                                                                                                                                                                                                              58106
                                                                                                                                                                                               14.4%;
                                                                                                               -EEVATCVGRNGYPIPQVIWYKNGRPLKE-EKNRVHIQSSQTVE
                                                                                                                                                                                    107;
                                                                                                                                                                                                                                              WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boynton
                                                                                                                                                                                                                                                                                                                                                                                            IG-LIKE V-TYPE DOMAIN.
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                               Score 485;
Pred. No. 1.
                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                             POTENTIAL.
A3616E9A2429E7B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain; Glycoprotein; Transmembrane
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.E.,
                                                                                                                                                                                                                                                                                                                                                                                               C2-TYPE DOMAIN
C2-TYPE DOMAIN
C2-TYPE DOMAIN
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                                                                                                                                                                                                . 2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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                                                                                                                                                                                             -29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              corresponds to activated
                                                                                                                                                                                                         Length 521;
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jaiswal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONTAINS
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                                                                                                                                                                                     Gaps
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PRESENTATION OF THE STATE OF TH
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046651;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CD166 ANTIGEN (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE) (ALCAM)
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                        DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                     EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differentiation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zaia J., Barry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bruder S.P., Ricalton N.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98215351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=MESENCHYME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALCAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mesenchymal stem cell surface antigen
leukocyte cell adhesion molecule and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314
                                                                                                                                                                                                                       PFAM; PF00047; ig; 4.
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                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bone Miner Res. 13:655-663(1998).
FUNCTION: CELL ADHESION MOLECULE
NEURITE EXTENSION BY NEURONS VIA
INTERACTIONS. MAY PLAY A ROLE IN
                                                                                                                                                                                                                                                                  C2-LIKE AND 2 V-LIKE |
L; Y13243; CAA73695.1;
P; Q13740; 1KJC.
                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN NEURINE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF THE NERVOUS SYSTEM. MAY BE INVOLVED IN OSTEOGENESIS. MAY PLAY AN IMPORTANT ROLE IN THE DEVELOPMENT OF A VARIETY OF MESENCHYMAL
                                                                                                                                                                                                                                                                                                                        TISSUES (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE
SUMILARITY: BELONGS TO THE
C2-LIKE AND 2 V-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ε
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATVVWMKDNIR--LRSSP--SFSSLQYQDAGNYVCETALQEVEGLKKRESLTLIVEGKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGDYKCSLIDKKSMIASTA----ITVHYL-DLSLNPSGEVTKQIGDALPVSCTISASRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDENR-EQVNHRATLIVGIVLRLLHGALVAGVVYWLYVKKSKTASKHVNKDLGNLEENKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STERKLPEPESRGVVIVAVIVCILVLAVLGAVLYFLY-KKGKLPCRRSGKQEITLPPSRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INSPEENVT-LTCTAENQLERTVNSLNVSAISI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QIKMTKKTDPSGLSKTIICHVEGFPKPAIQWTITGSGSVINQTEESPYINGRYYST--I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAFKERKVWVKENMVLNLSCEASGHPRPTISWNVNGTAS---EQDQDPQ---
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                                                                                                                                                                                                  adnesion;
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                                                                                                                                                                                                                                                IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata;
utheria; Lagomorpha; Leporidae; Oryctola
     <1
467
488
<1
<1
88
201
285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                     Immunoglobulin
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       466
487
521
58
165
259
337
                                                                                                                                                                                                                                                                                                                        DOMAINS
EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE DOMAIN.

IG-LIKE V-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                     domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                  I MEMBRANE PROTIMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is involved
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                                                                                                                                                                                                                                                                                                                                                  PROTEIN (BY SIMILARITY)
JLIN SUPERFAMILY. CONTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Connolly T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus
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                                                                                                                                                                                                     Transmembrane
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RESULT
Q9JHQ2
ID Q9
AC Q9
DT 01
DT 01
DT 01
DE ME
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Best Loc
Matches
                                                       O9JHQ2 PRELIMINARY;
O9JHQ2;
O1-OCT-2000 (TrEMBLrel. 15, C;
O1-OCT-2000 (TrEMBLrel. 15, L;
O1-OCT-2000 (TrEMBLrel. 15, L;
MELANOMA ADHESION MOLECULE (FI
                                    MCAM.
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CARBOHYD
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SEQUENCE
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CARBOHYD
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             musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGIPVNSKEP-----EVATCVGRNGYPIPQVIWYKNGRPLKEEKNRVHIQSSQTVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISPEENVT-LTCAAENQLERTVNSLNVSAISI----PE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAFKERKVWVKENMVLNLSCEASGHPRPTISWNVNGTAS---EQDDDPQ---RVLSTLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATVVWMKDNI--KLRSSP--SFSSLQYQDAGNYVCETALQEVEGLKKRESLTLIVEVKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEFQWLREETGQVLERGPVLQLHDLKREAGGGYRCVASVPSIPGLNRTQLVNVAIFGPPW |::: | | :::: | | ::::: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGNYKCSLIDKKSLIASTA----ITVHYL-DLSLNPXGELTKQIGDSLPVSCTISAIRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSGRYECQGLDLDTMISLLSEPQELLVNYVSDVRVSPAAP-ERQEGSSLTLTCEAESSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPKNAIKEGDNITLKCLGNGNPPPEEFFFYLPGQPEGIRSSNTYT-----LPNVRRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTQLYTMTSSLEYKTTKADIQTPFTCSITYYGPSGQKTVHSEQAVFDIYYPTEQVTIQVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -QIKMTKKTDPSGLSKTIICHVEGFPKPAIQWTITGSGSVINQTEESPYINGRYYS--KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPVGMLKEGDRVEIRCLADGNPPPH---FSISKONPSTREAEEETTNDNGVLVLEPARKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SGLYTLQSILKAQLVKEDKDAQFYCELNYRLPSGNHMKESREVTVPVFYPTEKVWLEV-: | | | | | | | | | : | ::|||:| ::|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EYKDRLNLSE-NYTLSISNARISDEKRFVCMLVTEDDVFEAPTVVKVFKQPSKPEIV---
                                                                                                                                                                                                                                                                                                                                      513
                                                                                                                                                                                                                                                                                                                                                                                        607
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                                                          Created)
Last sequence update)
Last annotation update)
(FRAGMENT).
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 465; DB Pred. No. 4.3e-
                                                                                                                                                                                                PRT;
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-28;
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Best Local S
Matches 70
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101-OCT-2000 (TrEMBLrel. 15, Cr
T 01-OCT-2000 (TrEMBLrel. 15, Lr
O1-OCT-2000 (TrEMBLREL. 15, Lr
TITHERAN GLYCOPROTEIN (FRAGM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.:
Best Local Similarity 90.9
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; C
Mammalia; Eutheria; C
Bovidae; Bovinae; Bos
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                EMBL; U89328;
NON_TER
SEQUENCE 86
                                                                                                                                                                                                                                                                                                                                                                                         Moore S.S., Byrne K.;
Submitted (FEB-1997) to the
EMBL; U89328; AAB66511.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAG-1998 (TrEMBLrel. 07, Last annotation update)
MELANOMA CELL ADHESION MOLECULE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Alais S., Allioli N., Vigneron P., Dunon D.;
"HEMCAM is the avian homologue of MCAM/CD146."
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
EMBL; AJ297451; CAB97363.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                             LAVLGAVLYFLYKKGKLPCRRSGKQEITLPPSRKSELVVEVKSDKLPEEMGLLQGSSGDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEMGLLQGSSGDKRAPGDQGEKYIDLRH
                                                                                                                                                                          RAPGDQGEKYIDLRH
                                                                                                                                                                                                                                LGLLGAVLYFFYKKGKLPCGRSGKQEITLPPSRKSEFVVEVKSDKLPEEMGLLQGSSGDK
                                                                                                                                                                                                                                                                                           l Similarity
70; Conserv
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                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                 Α,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9588 MW;
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Rodentia;
                                                                                                                                                                                                                                                                                                      10.8%;
                                                                                                                                                                                                      646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.1%;
90.9%;
                            (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                 WW.
                                      Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                      Score 362; DE Pred. No. 3.5e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 407; DB Pred. No. 1.1e 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                              F109345FDB2B3555 CRC64;
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                                                                                                   PRT;
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407; DB 11;
No. 1.1e-24;
                                                                                                 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Eute
minantia; Pecora;
                                                                                                                                                                                                                                                                                                      DB 6;
.5e-21;
                                                                                                                                                                                                                                                                                        4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovoidea;
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ALTERNATIVE PRODUCTS: TWO FORMS; ISOFORM F15G9.4A AND ISOFORM F15G9.4B (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

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076518
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                                                                                         SEQUENCE FROM N.A.

STRAIN-BRISTOL N2;

VOGEL B.E., Hedgecock E.M.;

Hemicentin is Required for Hemidesmosome Mediated Cell

"Hemicentin is Required for Hemidesmosome Mediated Cell

"Germ-Line Chromosome Segregation in C. elegans.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Selective Lutheran glycoprotein gene expression at barrier in normal brain and in human brain tumors.";
J. Cereb. Blood Flow Metab. 0:0-0(2000).
EMBL; AF270512; AAF81749.1; -.
NON_TER
1 1 1 SEQUIPMORE
                                       SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                  HIM-4 OR F15G9.4.
Caenorhabditis elegans.
                         Sulston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         076518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSELVVEVKSDKLPEEMGLLQGSS--GDKRAPGDQGEK 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTYGCRVEDFDVPEDAELSKTLELRVAYLDSLELS--AGEELSLPLHNSTTVTCSARGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRYECQGLDLDTMISL-LSEPQELLVNYVSDVRVSPAAPERQE---GSSLTLTCEAESSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GWVREGDSVQLLCQGDGSPTPEYTFFWLQDKQEDVLK-----TSLEGNLTLERVQRNQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMLKEGDRVEIRCLADGNPPPHFSI----SKQNPSTREAEEETTNDNGVLVLEPARKEHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STSTERKLPEPESRGVVIVAVIVCILVLAVLGAVLYFLYKKGKLPCRRSGKQEITLPPSR
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  (DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355
                       Kershaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                                                                             Nematoda;
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                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
EMBL/GenBank/DDBJ
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Pred. No. 3.3e-20;
3; Mismatches 155
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PFAM; PF00047; ig; 47.
PROSITE; PS00010 ASX_HYDROXYL; UNKNOWN_1.

R PROSITE; PS00402; PPD_TRANSP_INN_MEMBR; UNKN
R PROSITE; PS01186; EGF_2; UNKNOWN_1.

R PROSITE; PS01187; EGF_CA; 2.

KW Signal; Glycoprotein; EGF-like domain; Alte
FT SIGNAL
1 24 POTENTIAL.
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WORMPEP;
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hes 122;
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                                                                                                                                                             CVASVPSIPGLNRTQLVNV---AIFGPPWMAFKERKVWVKENMVLNLSCEASGHPRPTIS
TTLTPDSNTTT
                                                                                                                                                                                                                                                                                                   GLTLHFDSVSVKQEGNYHCVAQSKGNILDIDVELSVLAVP---IVGEDDNLEVF-----
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                                        WKIDGNDVDKSWLFDESLSLLRI---
                                                                             WNVNGTASEQDQDPQRVLSTLNVLVTPELLETG----VECTASNDLGKNTSTLFLELVNL
                                                                                                                        CRVT-NSAGKAERTLTLDVLEPPVFVEP--VFEANQKLIGNNPII-LQCQVTGNPKPTVI
                                                                                                                                                                                                               -LGKDISLSCDLQTESDDKTTFVWSINGSESDRPDNVQIPSDGHRLYITDAKPENNGKYM
                                                                                                                                                                                                                                                                                                                                          NGVLVLEPARKEHSGRYECOG-----LDLDTMISLLSEPQELLVNYVSDVRVSPAAPER
                                                                                                                                                                                                                                                                                                                                                                                                              FYPTEKVWLEVEPVGMLKEGDRVEIRCLADGNPPPHFSI----SKQNPSTREAEEETTND
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                                                                                                                                                                                                                                                          QEGSSLTLTC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLHVFKAK-ITDSGVYKCVA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --EPNIQVNPLGIPVNSKEPEEVATCVGRNGYPIPQVIWYKNGRPL-----KEEKN
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Z47070;
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CAA87344.1;
                                                                                                                                                                                                                                            -EAESSQDLEFQWL------REETGQVLERGPVLQLHDLKREAGGGYR
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22.1%;
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MW; DA8511FF2B58D37B CRC64;
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l; Mismatches
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Pred. No.
                                      ·EKL-TGKSAQISCTAENKAGTASRDFFIQNIAA
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Db 1826 PTFKNEGDQET 1836

Search completed: March 23, 2001, 12:32:35 Job time: 113 sec